

Additional results

1. A comparison between the results of the analysis of association for back pain using UK Biobank release v2 and v3

The second release of UK Biobank data has been reported to be having issues with imputation of SNPs based on UK10K+1000G panel (<https://www.ukbiobank.ac.uk/2017/07/important-note-about-imputed-genetics-data/>). This has been fixed for the 3rd release of UK Biobank data. Our study has been carried out months before the 3rd release; therefore, in our study we only analysed SNPs imputed using HRC panel for which no issues have been reported. In a response to a query risen by an anonymous reviewer of our manuscript, we used the 3rd release data to carry out an analysis of association for SNPs on chromosomes 8, 10, and 12 that we found associated with BP in the current study.

The results appeared to be fully equivalent for the regions on chromosomes 8 and 10 associated with BP in the current study (Table) with the minute differences in P-values explained by the fact that in v3 there were 2 persons less due to data withdrawal. On chromosome 12, the lead SNPs were different (rs12310519 and rs7303462 for the 2nd and 3rd releases, respectively); however, they are located 308bp apart and are in perfect LD ($r^2=1$). The lead SNP rs12310519 in the 2nd release is second best after rs7303462 in the 3rd release.

Table – A comparison of the results of the analysis of the 2nd and 3rd releases of the UK Biobank

Locus	UKBB release version	Lead SNP	Chr:Pos	Beta (SE)	P-value
<i>GSDMC/CCDC26</i>	v2	rs7814941	8:130718859	0.046 (0.007)	1.81×10^{-11}
	v3	rs7814941	8:130718859	0.046 (0.007)	1.83×10^{-11}
<i>SPOCK2/CHST3</i>	v2	rs3180	10:73820622	-0.037 (0.006)	7.83×10^{-12}
	v3	rs3180	10:73820622	-0.037 (0.005)	7.74×10^{-12}
<i>SOX5</i>	v2	rs12310519	12:23975219	-0.056 (0.007)	1.38×10^{-14}
	v3	rs7303462	12:23974911	-0.058 (0.007)	1.83×10^{-15}

2. *SPOCK2* vs *CHST3* as the most likely candidate gene for BP on chromosome 10 (lead SNP rs3180)

The genes lie in different LD-blocks [4] and COJO analysis identified a single association signal in the region with rs3180 being the lead SNP. This and nearby SNPs serve as eQTL for both *SPOCK2* and *CHST3*, depending on the tissue type according to the GTEx database [1]. The specific pattern of the expression of *SPOCK2* and *CHST3* gene could result from a functional variant in a tissue-specific transcription factor binding site. Apart from rs3180, a range of other SNPs located in the region exhibited tissue-specific effects on the expression of the two genes [1]. The 99% credible set of SNPs defined by PAINTOR software [2] for this region included 7 potentially causal variants (rs2091331, rs1006974, rs6480592, rs1269600, rs1668159, rs1668169, rs896074; Supplementary Table 9A) of which two SNPs (rs2091331 and rs1006974) were classified as regulatory region variants by the VEP [3] (Supplementary

Table 9B). According to Regulatory Elements DB [5], these two variants are located less than 500bp apart from the nearest DNaseI hypersensitivity sites (DHS) that significantly correlate with *SPOCK2* and *CHST3*. In particular, rs1006974 is located 144 bp apart from DHS #331668 (chr10: 73745620-73745770) which is correlated significantly both with *SPOCK2* and *CHST3*. The top five binding transcription factors for this site were *TAL1::TCF3*, *Prrx2*, *ARID3A*, *Pdx1*, and *HNF1A*.

Given that rs3180 is an eQTL we tested its causal and pleiotropic effects on BP using blood eQTL data [6] and eQTL data for 44 tissues as provided in the GTEx database [1] coupled with summary data-based Mendelian randomization (SMR) analysis and heterogeneity in dependent instruments (HEIDI) method [7]. In short, the first method tests for the association between the traits of interest (eQTLs) mediated by a locus, and the second test checks whether both traits are affected by the same underlying causal variant. For the blood eQTL data [6], we observed statistically significant SMR statistics for *SPOCK2* gene ($p_{smr}=1e-8$), indicating the association between BP and expression level mediated by the locus. Subsequent HEIDI test showed no difference in association patterns ($p_{heidi}=0.1$), suggesting *SPOCK2* as a strong candidate gene for BP in the rs3180 locus. The SMR coefficient was positive ($b=5.9$), consistent with a potential causal variant in this region increasing the risk of BP and the level of *SPOCK2* gene expression. For GTEx data, the SMR coefficient was statistically significant for rs3180 in testis, muscle skeletal and adrenal gland tissues, but HEIDI test showed no difference in association pattern for this SNP in testis tissue for *CHST3* gene ($p_{heidi}=0.06$). The SMR coefficient was positive for this probe ($b_{smr}=6.3$). For muscle skeletal and adrenal gland tissues the HEIDI p-values located in “grey zone” where we feel no confidence either to claim the similarity between associations (pleiotropy) or to reject the hypothesis of pleiotropy ($p_{heidi} = 0.01$ and 0.04 respectively). Thus, in contrast with the eQTL data for blood, this suggests *CHST3* as the candidate gene for BP at this locus.

Taken together, the available data suggest the presence of a true functional variant associated with BP in this region; however, we cannot identify with confidence what gene – *SPOCK2* or *CHST3* – is the most likely candidate.

References

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- [7] Zhu Z, Zhang F, Hu H, Bakshi A, Robinson MR, Powell JE, Montgomery GW, Goddard ME, Wray NR, Visscher PM, Yang J. Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. *Nat Genet* 2016;48(5):481-487.

Supplementary Methods

Testing for pleiotropy using SMR/HEIDI approach

SMR/HEIDI analysis was conducted as described by Zhu et al.¹ HEIDI statistics was calculated as

$$T_{HEIDI} = \sum_i^m z_{d(i)}^2, \text{ where } m \text{ is the number of SNPs selected for analysis, } z_{d(i)} = \frac{d_i}{SE_{(d_i)}} \text{ and } d_i = \beta_{SMR_i} - \beta_{SMR \text{ (lead SNP)}}.$$

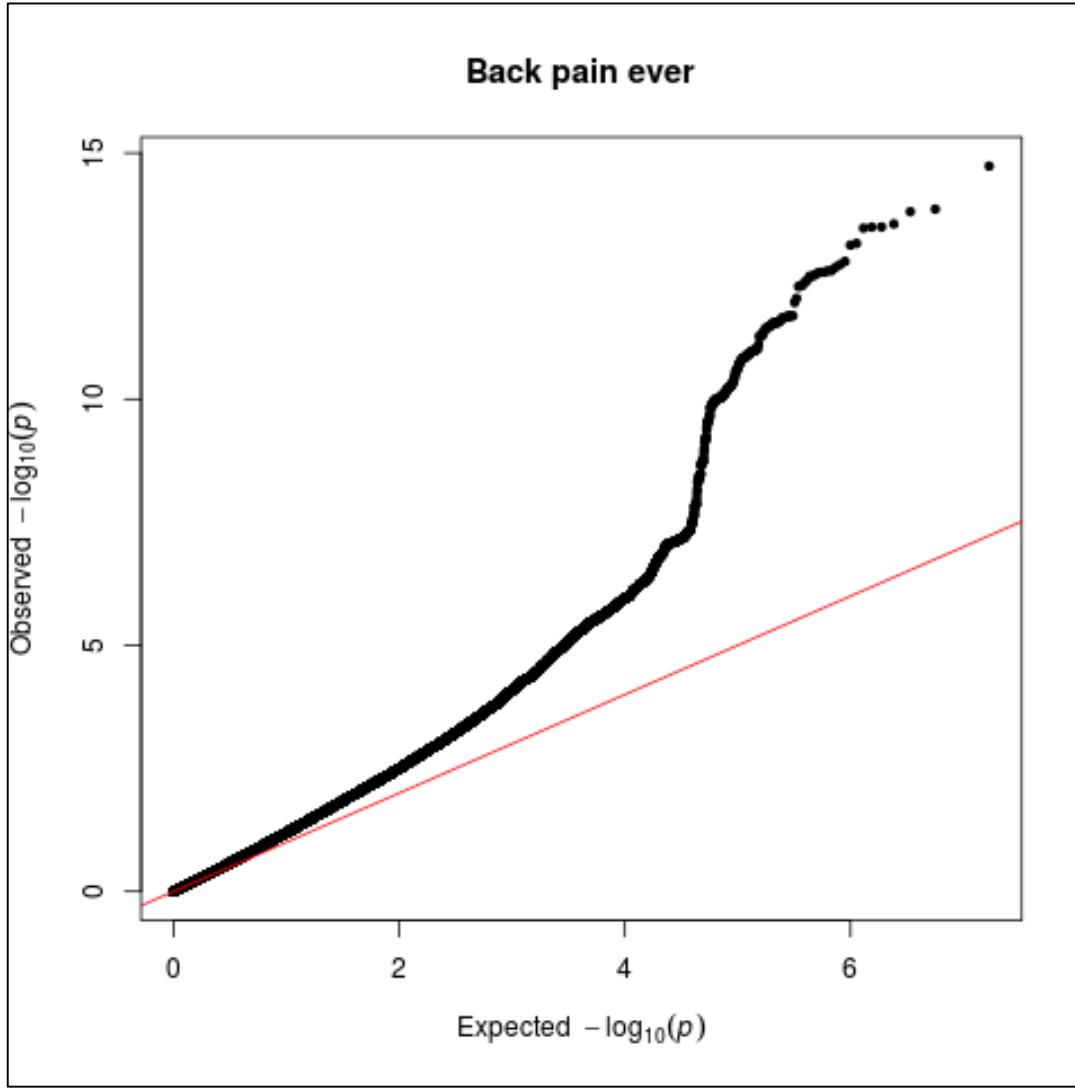
SNP selection was performed as follows:

- 1) We defined a set of eligible markers within ± 250 kb from the lead SNP in the primary GWAS, which had $\chi^2 > 10$ in the primary GWAS, and for which the results were reported in the secondary GWAS;
- 2) Made empty “target” and “rejected” SNP sets;
- 3) Selected SNP from the primary GWAS with the lowest P ;
- 4) If this SNP had $r^2 > 0.9$ with any SNP in the target SNP set, we added it to the “rejected” set. LD matrix (r^2) was computed with PLINK 1.9 (<https://www.cog-genomics.org/plink2>) using 1000 Genomes data for 503 European individuals (<http://www.internationalgenome.org/data/>);
- 5) Otherwise, it was added to the “target” set;
- 6) Procedure was repeated from the step 3) until either eligible SNP set was exhausted, or the “target” set had 20 SNPs. If we could not select 3 or more SNPs, no test was performed.

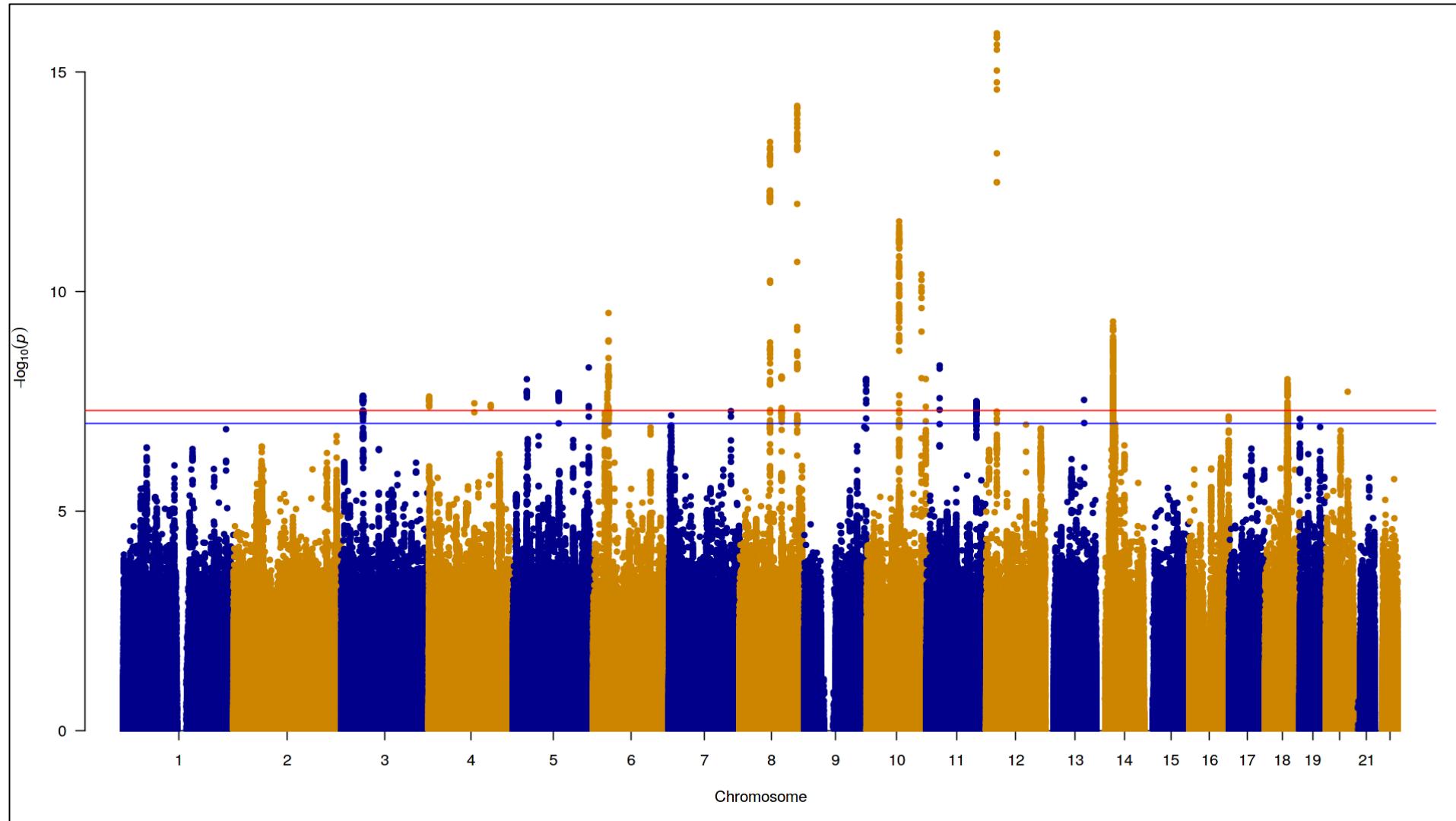
GWAS summary statistics for VVs was obtained from the Gene ATLAS database (I83_GA). Analysis was conducted using Python 3.5 as the main programming language.

REFERENCES:

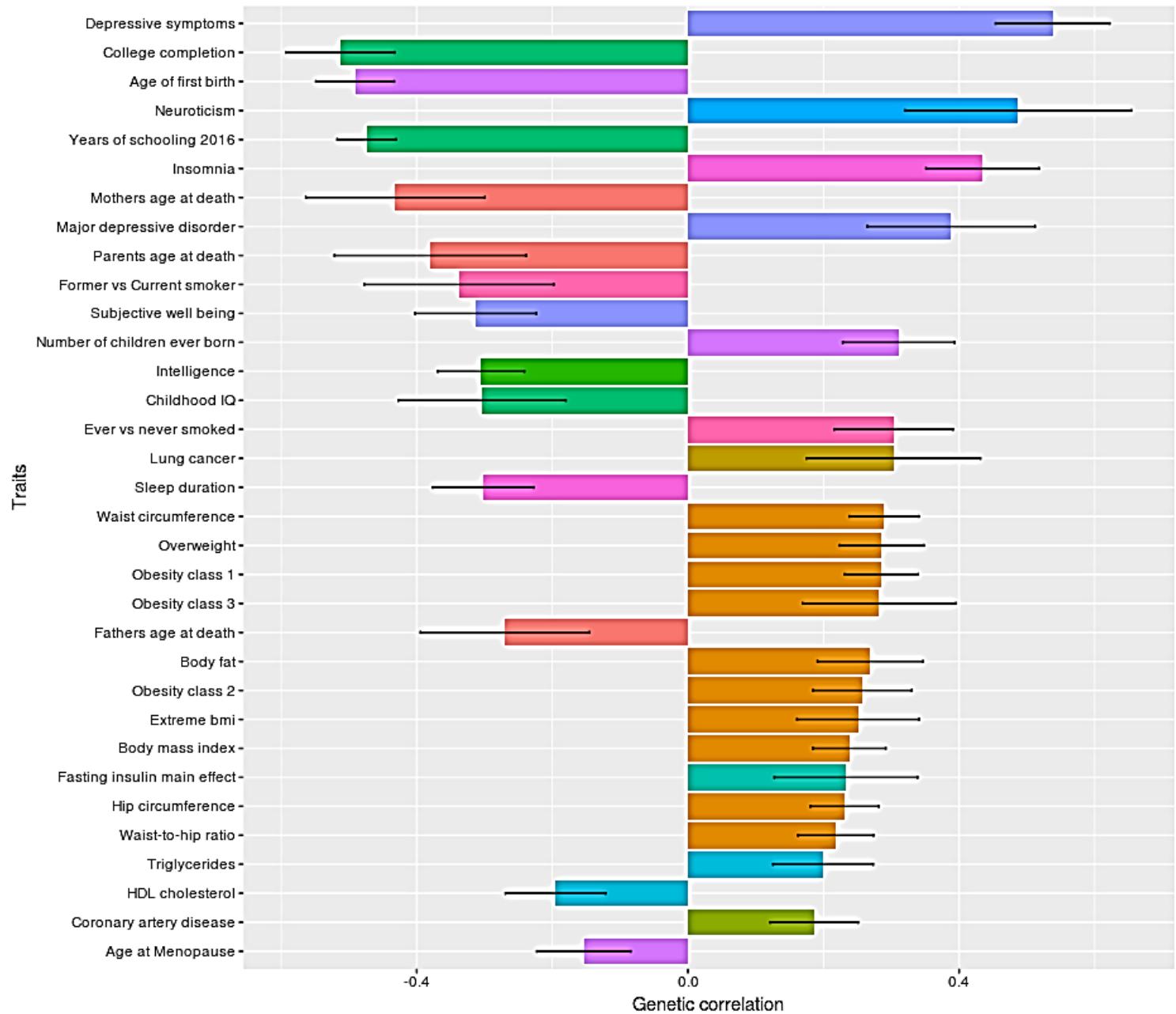
1. Zhu, Z. et al. Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. *Nat. Genet.* **48**, 481–7 (2016). doi:10.1038/ng.3538



Supplementary Figure 1 – QQ plot for discovery GWAS

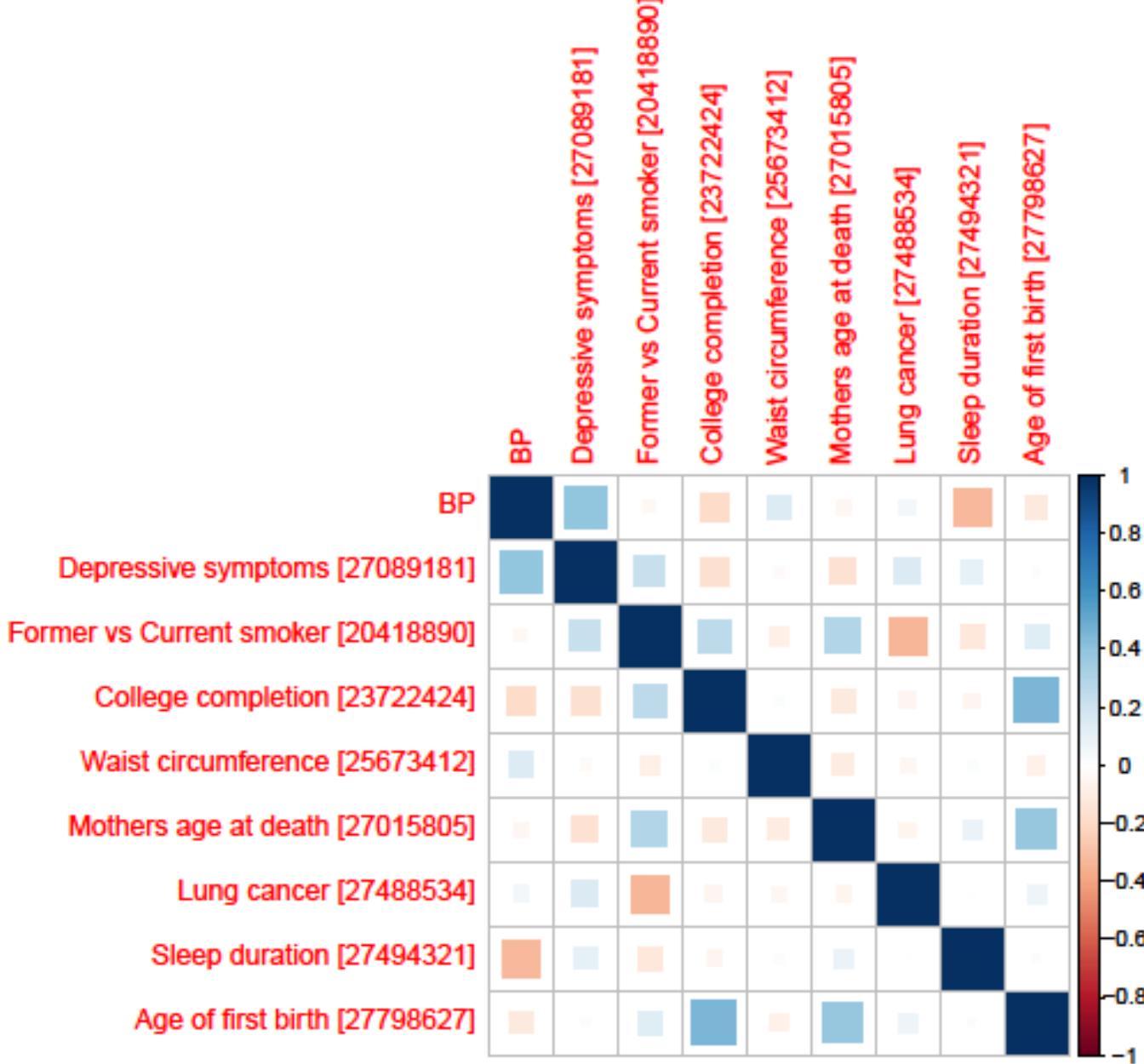


Supplementary Figure 2 – Manhattan plot of meta-analysis GWAS of discovery and replication samples from the UK Biobank (N=453,862). Red line corresponds to the genome-wide significance threshold of 5×10^{-8} , while blue line corresponds to the suggestive association threshold of 5×10^{-7} .



Supplementary Figure 3 – Barplots of genetic correlations between back pain and complex traits showing statistical significance ($p < 4.3 \times 10^{-5}$).

Supplementary Figure 4 - Heatmap of partial genetic correlations for 16 traits including BP.



Supplementary Table 1. Information about discovery and replication cohorts.

		Discovery	Replication	p-value		
Age		57.05 (8.02)	57.07 (8.00)	0.513		
BMI		27.41 (4.75)	27.44 (4.78)	0.247		
Sex, 1/2		160808 / 189192	26783 / 31460	0.862		
Group	Ethnicity	Total	Cases	Controls	Cases/Controls	Prevalence
Discovery	British EA	350000	91100	258900	0.352	0.260
Replication	British and other EA	103862	28284	75578	0.374	0.272
Replication	South Asian	7159	2520	4639	0.543	0.352
Replication	African	7259	2414	4845	0.498	0.333
Replication	Chinese	1485	401	1084	0.370	0.270

Supplementary Tables 2. Results of molecular pleiotropy analysis in regions with significant association to BP.

Tables

- A) List of risk factors for BP
- B) List of tissues for GTEx
- C) SMR-HEIDI results for eQTLs (westra and GTEx v6).
- D) SMR-HEIDI results for seventeen risk factors.

Coloring:

Green	Significant SMR and p-value_heidi>0.01
Pail green	Suggestively significant SMR and p-value_heidi>0.01
Orange	Significant SMR and p-value_heidi<0.01

Legend for A and B tables

Name	Description
beta_smr	MR beta
gwas_1	Name of GWAS 1 (BP)
gwas_2	Name of GWAS 2 (probe name or trait name)
locus	Locus name
n_heidi	Number of SNPs in HEIDI test
p_heidi	P-value of HEIDI test
p_smr	P-value of SMR test
sigma_smr	Sigma of MR beta
snps_heidi	The list of SNPs in HEIDI test
a1_REF	Allele 1
a2_REF	Allele 2
bp_REF	Position of SNP for which MR beta was computed
chr_REF	Chromosome of SNP for which MR beta was computed
rsid_REF	rsid of SNP for which MR beta was computed
Gene_G2	Gene name for probe (for A and B tables)
Probe_Ch_G2	Probe chromosome
Probe_G2	Probe name ID
Probe_bp_G2	Probe position
SE_G2	Standard error of beta of SNP for which MR beta was computed on GWAS 2
b_G2	Beta of SNP for which MR beta was computed on GWAS 2
p_G2	Log of p-value for GWAS 2
data	Data set for eQTLs (westra or GTExv6)
tissue	Tissue for eQTLs

Supplementary Tables 2A. Risk factors, behavior and environment factors, associated with BP.

LEGEND

Rg with BP Genetic correlation of given trait with BP

P-value of Rg P-value of genetic correlation

Proxy trait w/ The name of proxy trait for which GWAS was available for EUR population

	Trait name	in UKBB or eGAP	Proxy trait w/ Reference	Sample size	Number of ca #	Rg with BP	P-value of Rg
Risk Factors	Osteoarthritis	+ null number of	ported osteoarthritis http://geneat	408455	34791	1	0.55 7.49E-41
	Fibromyalgia	-	-	-	-	-	-
	Degenerative disc phenotype	+	Disc problems http://geneat	408455	7823	2	0.77 6.71E-24
	Osteoporosis	+	ported osteoporosis http://geneat	408455	6539	3	0.04 4.49E-01
	Scoliosis	+	M41 Scoliosis http://geneat	408455	1051	4	0.35 1.09E-03
	Smoking	+	Smoking status http://geneat	408455	-	5	0.35 7.30E-42
	Height	+	Standing height http://geneat	408455	-	6	0.03 8.32E-02
	BMI	+	BMI http://geneat	408455	-	7	0.33 1.97E-56
	Well being	+	Happiness (neal) http://www.r	110935	-	8	-0.16 1.79E-04
	Intelligence	+	Intelligence score http://www.r	108818	-	9	-0.32 3.49E-30
Behavior and enviro	Education attainment	+	Education: Year of Ed doi:10.1038/r	328917	-	10	-0.47 7.12E-101
	Anorexia nervosa	null number of	-	-	-	-	-
	Anxiety	+	Anxiety/panic attack http://geneat	408455	5664	11	0.21 5.97E-04
	MDD	+	Major depression http://geneat	408455	23538	12	0.44 1.33E-23
		+	5_NEUROTICIS doi:10.1038/r	17375	-	13	0.74 3.39E-02
		+	5_CNSCIENTIOUS doi:10.1038/r	17375	-	14	-0.12 2.59E-01
	Big five	+	5_EXTRAVERSION doi:10.1038/r	17375	-	15	-0.33 6.06E-02
		+	5_AGREEABLENESS doi:10.1038/r	17375	-	16	-0.86 2.17E-01
		+	5_OPENNES doi:10.1038/r	17375	-	17	-0.19 1.92E-02

Supplementary Table 2B. List of tissues for GTEx analysis.

#	Tissue
1	Adipose subcutaneous
2	Adipose visceral omentum
3	Adrenal gland
4	Artery aorta
5	Artery coronary
6	Artery tibial
7	Brain anterior cingulate cortex BA24
8	Brain caudate basal ganglia
9	Brain cerebellar hemisphere
10	Brain cerebellum
11	Brain cortex
12	Brain frontal cortex BA9
13	Brain hippocampus
14	Brain hypothalamus
15	Brain nucleus accumbens basal ganglia
16	Brain putamen basal ganglia
17	Breast mammary tissue
18	Cells EBV-transformed lymphocytes
19	Cells transformed fibroblasts
20	Colon sigmoid
21	Colon transverse
22	Esophagus gastroesophageal junction
23	Esophagus mucosa
24	Esophagus muscularis
25	Heart atrial appendage
26	Heart left ventricle
27	Liver
28	Lung
29	Muscle skeletal
30	Nerve tibial
31	Ovary
32	Pancreas
33	Pituitary
34	Prostate
35	Skin not sun exposed suprapubic
36	Skin sun exposed lower leg
37	Small intestine terminal ileum
38	Spleen
39	Stomach
40	Testis
41	Thyroid
42	Uterus
43	Vagina
44	Whole blood

Supplementary Table 2C. Results of SMR/HEIDI analysis for eQTLs

locus	gwas_2	n_heidi	p_heidi	beta_smr	p_smr	sigma_smr	gene_name	tissue	data	a1_REF	a2_REF	bp_REF	chr_REF	rsid_REF	beta_G2	p_G2	probe_G2
rs3180	westra_ILMN_1656287	18	0.098416	5.922	1E-08	1.03335 SPOCK2	blood	westra	A	G	73761015	10	rs751450	-0.20074	23.83004	ILMN_1656287	
rs7814941	Esophagus mucosa_ENSG0000122863.5	20	6.82E-09	13.560	3E-08	2.44706 GSDMC	Esophagus	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.602051	12.72701	ENSG00000147697.4	
rs3180	Adrenal gland_ENSG0000010122863.5	20	0.040039	-20.592	1.33E-07	3.903538 SPOCK2	Adrenal gl	GTEx_v6	T	C	73762673	10	rs2219837	0.702177	11.92649	ENSG00000107742.8	
rs7814941	Skin sun exposed lower leg_EI	20	2.29E-07	6.919	7.61E-07	1.399241 GSDMC	Skin sun ex	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.307215	9.142575	ENSG00000147697.4	
Threshold SMR									2.97E-05								
rs3180	westra_ILMN_1685097	17	5.1E-06	-3.007	3.56E-05	0.727322 ASCC1	blood	westra	A	G	73761015	10	rs751450	0.101941	6.599519	ILMN_1685097	
rs7814941	Esophagus mucosa_ENSG0000122863.5	20	2.02E-05	-8.951	4.28E-05	2.187527 RP11-274N	Esophagus	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.39743	5.531123	ENSG00000224110.3	
rs3180	Testis_ENSG00000122863.5	20	0.068347	6.338	5.49E-05	1.57123 CHST3	Testis	GTEx_v6	T	C	73762673	10	rs2219837	-0.21613	5.615229	ENSG00000122863.5	
rs3180	Muscle skeletal_ENSG0000010122863.5	20	0.014297	-9.570	8.74E-05	2.43924 SPOCK2	Muscle ske	GTEx_v6	T	C	73762673	10	rs2219837	0.32632	5.5112	ENSG00000107742.8	
rs7814941	Muscle skeletal_ENSG0000010122863.5	20	3.17E-07	6.002	0.00012	1.560365 GSDMC	Muscle ske	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.266505	4.875479	ENSG00000147697.4	
rs3180	Cells EBV-transformed lympho	20	0.155224	-17.067	0.000173	4.543961 CHST3	Cells EBV-t	GTEx_v6	T	C	73762673	10	rs2219837	0.581969	4.638155	ENSG00000122863.5	
Suggestive threshold SMR									0.000297								
rs3180	Esophagus mucosa_ENSG0000122863.5	20	0.047796	-7.611	0.000467	2.175212 CHST3	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	0.259551	4.135004	ENSG00000122863.5	
rs7814941	Skin sun exposed lower leg_EI	20	2.34E-05	-5.932	0.00075	1.759948 RP11-274N	Skin sun ex	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.2634	3.643479	ENSG00000224110.3	
rs3180	Heart left ventricle_ENSG0000122863.5	20	0.023768	-9.291	0.000796	2.770016 SPOCK2	Heart left v	GTEx_v6	T	C	73762673	10	rs2219837	0.316825	3.726277	ENSG00000107742.8	
rs3180	Thyroid_ENSG00000148719.1	20	0.074392	4.753	0.000877	1.428349 DNAJB12	Thyroid	GTEx_v6	T	C	73762673	10	rs2219837	-0.16206	3.715569	ENSG00000148719.10	
rs3180	Pancreas_ENSG00000122863.	20	0.062943	8.546	0.000925	2.579813 CHST3	Pancreas	GTEx_v6	T	C	73762673	10	rs2219837	-0.29141	3.575816	ENSG00000122863.5	
rs7814941	Heart left ventricle_ENSG0000122863.5	19	0.000388	5.680	0.000978	1.722866 GSDMC	Heart left v	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.252183	3.426923	ENSG00000147697.4	
rs7814941	Thyroid_ENSG00000147697.4	20	0.003203	4.978	0.001277	1.545459 GSDMC	Thyroid	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.221023	3.313432	ENSG00000147697.4	
rs3180	Colon sigmoid_ENSG00000122863.5	20	0.312484	-9.737	0.001545	3.075343 CHST3	Colon signr	GTEx_v6	T	C	73762673	10	rs2219837	0.33203	3.241252	ENSG00000122863.5	
rs3180	Artery tibial_ENSG00000107742.8	20	0.350199	-5.981	0.001856	1.92174 SPOCK2	Artery tibi	GTEx_v6	T	C	73762673	10	rs2219837	0.203955	3.225624	ENSG00000107742.8	
rs3180	Ovary_ENSG00000107742.8	20	0.040329	-12.091	0.002075	3.926677 SPOCK2	Ovary	GTEx_v6	T	C	73762673	10	rs2219837	0.412308	2.979047	ENSG00000107742.8	
rs3180	Adrenal gland_ENSG0000013803.13	20	0.419369	-8.381	0.002175	2.734131 ASCC1	Adrenal gl	GTEx_v6	T	C	73762673	10	rs2219837	0.28578	3.039506	ENSG0000013803.13	
rs3180	Colon sigmoid_ENSG00000214688.4	20	0.002626	13.223	0.002176	4.314211 C10orf105	Colon signr	GTEx_v6	T	C	73762673	10	rs2219837	-0.45092	3.036459	ENSG00000214688.4	
rs7814941	Spleen_ENSG00000254223.1	17	0.051082	12.409	0.00226	4.0635 RP11-419K Spleen	Spleen	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.550953	2.835145	ENSG00000254223.1	
rs3180	westra_ILMN_1712929	6	0.27868	-5.055	0.00249	1.671256 DNAJB12	blood	westra	T	C	73858549	10	rs1668156	0.094524	5.796187	ILMN_1712929	
rs3180	westra_ILMN_1832720	11	0.06255	-2.702	0.002693	0.900438 HS.46555	blood	westra	G	T	73804761	10	rs1632171	0.069983	3.515138	ILMN_1832720	
rs3180	Esophagus mucosa_ENSG0000122863.5	20	0.030179	6.120	0.003182	2.074846 MICU1	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	-0.20869	2.879163	ENSG00000107745.12	
rs3180	Brain hypothalamus_ENSG0000122863.5	20	0.079138	-10.438	0.003189	3.539618 C10orf54	Brain hypc	GTEx_v6	T	C	73762673	10	rs2219837	0.355933	2.726624	ENSG00000107738.15	
rs3180	westra_ILMN_2333865	6	0.631428	-4.566	0.003769	1.576087 DNAJB12	blood	westra	T	C	73858549	10	rs1668156	0.08538	4.831553	ILMN_2333865	
rs7814941	Brain anterior cingulate cortex	16	0.182551	4.246	0.004058	1.477702 FAM49B	Brain ante	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.188539	2.488035	ENSG00000153310.14	
rs3180	Esophagus mucosa_ENSG0000122863.5	20	0.230417	4.510	0.004174	1.57449 MCU	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	-0.15381	2.716986	ENSG00000156026.10	
rs3180	westra_ILMN_1781098	1	NA	-6.557	0.004389	2.301639 DNAJB12	blood	westra	C	T	74046212	10	rs1076250	-0.1095	7.315436	ILMN_1781098	
rs3180	Esophagus muscularis_ENSG0000122863.5	20	0.113675	-5.122	0.004479	1.802116 SPOCK2	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	0.174663	2.668067	ENSG00000107742.8	
rs3180	westra_ILMN_1783149	14	1.48E-05	1.795	0.00498	0.639119 CDH23	blood	westra	A	G	73761015	10	rs751450	-0.06085	2.673689	ILMN_1783149	
rs3180	Skin not sun exposed suprapu	20	0.064108	5.552	0.005308	1.991603 UNC5B	Skin not su	GTEx_v6	T	C	73762673	10	rs2219837	-0.18933	2.561385	ENSG00000107731.8	
rs7814941	Brain caudate basal ganglia_E	18	0.215072	-9.568	0.005797	3.467861 RP11-473C	Brain caud	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.42482	2.377804	ENSG00000253720.1	
rs3180	Artery tibial_ENSG00000122863.5	20	0.424065	-3.371	0.005914	1.224585 CHST3	Artery tibi	GTEx_v6	T	C	73762673	10	rs2219837	0.114941	2.521444	ENSG00000122863.5	
rs3180	Cells transformed fibroblasts	20	0.258794	3.741	0.006294	1.369401 DNAJB12	Cells trans	GTEx_v6	T	C	73762673	10	rs2219837	-0.12758	2.483071	ENSG00000148719.10	
rs3180	Heart left ventricle_ENSG0000122863.5	20	0.034238	6.026	0.006345	2.207692 DNAJB12	Heart left v	GTEx_v6	T	C	73762673	10	rs2219837	-0.20548	2.457255	ENSG00000148719.10	
rs3180	Adrenal gland_ENSG00000272630.1	8	0.135098	-20.166	0.00642	7.399142 RP11-344N	Adrenal gl	GTEx_v6	T	C	73865131	10	rs1100017	0.375094	3.665291	ENSG00000272630.1	
rs7814941	Spleen_ENSG00000147697.4	17	0.002273	-9.317	0.006725	3.437906 GSDMC	Spleen	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.41369	2.286079	ENSG00000147697.4	
rs3180	Cells transformed fibroblasts	20	0.070637	-2.512	0.007223	0.934945 CHST3	Cells trans	GTEx_v6	T	C	73762673	10	rs2219837	0.085646	2.404124	ENSG00000122863.5	
rs3180	Adrenal gland_ENSG00000148719.10	20	0.533158	-7.738	0.0073	2.884127 DNAJB12	Adrenal gl	GTEx_v6	T	C	73762673	10	rs2219837	0.263852	2.351341	ENSG00000148719.10	
rs3180	Thyroid_ENSG00000122863.5	20	0.710256	4.041	0.008644	1.539062 CHST3	Thyroid	GTEx_v6	T	C	73762673	10	rs2219837	-0.13781	2.303326	ENSG00000122863.5	
rs3180	westra_ILMN_1807540	1	NA	-4.975	0.009362	1.914712 CBARA1	blood	westra	C	T	74046212	10	rs1076250	-0.08309	4.451847	ILMN_1807540	
rs3180	Cells EBV-transformed lympho	20	0.02841	-9.124	0.009951	3.539682 MCU	Cells EBV-t	GTEx_v6	T	C	73762673	10	rs2219837	0.311114	2.17465	ENSG00000156026.10	

rs3180	Whole blood_ENSG000001487	20	0.06839	2.028	0.010256	0.790122	DNAJB12	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	-0.06916	2.214162	ENSG00000148719.10
rs3180	Esophagus muscularis_ENSG0	20	0.64433	4.393	0.011268	1.733498	DNAJB12	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.14981	2.146204	ENSG00000148719.10
rs7814941	Esophagus mucosa_ENSG0000	20	0.01049	-4.822	0.012241	1.925015	RP11-419K	Esophagus	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.21411	2.056092	ENSG00000254223.1
rs3180	Colon transverse_ENSG00000	20	0.045981	2.800	0.012247	1.117891	CHST3	Colon tran	GTEEx_v6	T	C	73762673	10	rs2219837	-0.09549	2.086923	ENSG00000122863.5
rs3180	Small intestine terminal ileum	20	0.678207	-9.955	0.012837	4.00075	SLC29A3	Small intes	GTEEx_v6	T	C	73762673	10	rs2219837	0.339462	1.995636	ENSG00000198246.7
rs3180	Uterus_ENSG00000107738.15	20	0.769727	9.310	0.012913	3.744834	C10orf54	Uterus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.31748	1.979556	ENSG00000107738.15
rs3180	Brain hypothalamus_ENSG000	20	0.107989	-9.390	0.013432	3.798471	C10orf105	Brain hypc	GTEEx_v6	T	C	73762673	10	rs2219837	0.320206	1.980306	ENSG00000214688.4
rs3180	Colon transverse_ENSG00000	20	0.845136	8.966	0.013665	3.635886	RP11-354E	Colon tran	GTEEx_v6	T	C	73762673	10	rs2219837	-0.30574	2.028434	ENSG00000272627.1
rs3180	Cells EBV-transformed lympho	20	0.363962	10.755	0.014138	4.38317	RP11-570C	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	-0.36675	1.990294	ENSG00000226701.1
rs3180	Pancreas_ENSG00000107742.	20	0.181584	-7.970	0.014374	3.255817	SPOCK2	Pancreas	GTEEx_v6	T	C	73762673	10	rs2219837	0.27176	1.993329	ENSG00000107742.8
rs3180	Skin sun exposed lower leg_EI	20	0.0053	3.160	0.015026	1.299374	ASCC1	Skin sun e	GTEEx_v6	T	C	73762673	10	rs2219837	-0.10775	2.000611	ENSG00000138303.13
rs3180	Breast mammary tissue_ENSG	20	0.023751	-8.653	0.015075	3.560123	RP11-354E	Breast mai	GTEEx_v6	T	C	73762673	10	rs2219837	0.295073	1.98068	ENSG00000272627.1
rs3180	Lung_ENSG00000214688.4	20	0.087436	5.778	0.015107	2.377897	C10orf105	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	-0.19702	1.995283	ENSG00000214688.4
rs3180	Brain cerebellum_ENSG00000	20	0.076581	10.535	0.015609	4.356916	RP11-354E	Brain cere	GTEEx_v6	T	C	73762673	10	rs2219837	-0.35923	1.930676	ENSG00000272627.1
rs3180	Esophagus muscularis_ENSG0	20	0.307958	2.738	0.015621	1.132593	ASCC1	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.09337	1.969574	ENSG00000138303.13
rs7814941	Heart left ventricle_ENSG0000	19	0.382693	5.924	0.0173	2.488608	RP11-473C	Heart left \	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.263007	1.870333	ENSG00000254317.1
rs7814941	Spleen_ENSG00000254263.1	17	0.574367	-10.435	0.017815	4.403961	RP11-473C	Spleen	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.46331	1.813397	ENSG00000254263.1
rs3180	Brain anterior cingulate cortex	16	0.651771	-5.795	0.018352	2.457326	RPL17P50	Brain ante	GTEEx_v6	A	G	73820622	10	rs3180	0.192988	1.811325	ENSG00000213700.3
rs3180	Artery aorta_ENSG000001228	20	0.008386	4.061	0.019982	1.745593	CHST3	Artery aor	GTEEx_v6	T	C	73762673	10	rs2219837	-0.1385	1.835347	ENSG00000122863.5
rs3180	Spleen_ENSG00000122884.8	8	0.923638	-14.252	0.020677	6.159379	P4HA1	Spleen	GTEEx_v6	T	C	73858549	10	rs1668156	0.266508	2.268008	ENSG00000122884.8
rs3180	Colon transverse_ENSG00000	20	0.498616	-5.267	0.021057	2.283049	MICU1	Colon tran	GTEEx_v6	T	C	73762673	10	rs2219837	0.179601	1.801489	ENSG00000107745.12
rs3180	Lung_ENSG00000107742.8	20	0.265246	-3.041	0.022133	1.329075	SPOCK2	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	0.103699	1.791645	ENSG00000107742.8
rs3180	Brain cortex_ENSG000001228	20	0.422846	4.412	0.022143	1.928374	CHST3	Brain cort	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15045	1.748143	ENSG00000122863.5
rs3180	Prostate_ENSG00000107738.:	20	0.002227	-5.921	0.022869	2.601974	C10orf54	Prostate	GTEEx_v6	T	C	73762673	10	rs2219837	0.20191	1.724868	ENSG00000107738.15
rs3180	Adipose visceral omentum_E	20	0.847973	3.926	0.024214	1.742041	UNC5B-AS	Adipose vi	GTEEx_v6	T	C	73762673	10	rs2219837	-0.13388	1.733178	ENSG00000237512.2
rs12310519	Pituitary_ENSG00000134532.:	11	0.694054	3.958	0.025456	1.771374	SOX5	Pituitary	GTEEx_v6	C	T	23982559	12	rs9804988	-0.22917	1.629822	ENSG00000134532.11
rs3180	Adipose subcutaneous_ENSG0	20	0.047595	-4.618	0.025489	2.067013	SPOCK2	Adipose su	GTEEx_v6	T	C	73762673	10	rs2219837	0.157457	1.719199	ENSG00000107742.8
rs3180	Heart atrial appendage_ENSG	8	0.158911	7.578	0.02645	3.41433	P4HA1	Heart atria	GTEEx_v6	T	C	73858549	10	rs1668156	-0.14171	2.102178	ENSG00000122884.8
rs3180	Brain caudate basal ganglia_E	20	0.223035	-5.391	0.026762	2.434073	CHST3	Brain caud	GTEEx_v6	T	C	73762673	10	rs2219837	0.183847	1.656893	ENSG00000122863.5
rs3180	Brain anterior cingulate cortex	20	0.037024	14.493	0.027846	6.589334	RP11-150C	Brain ante	GTEEx_v6	T	C	73762673	10	rs2219837	-0.49421	1.609697	ENSG00000272988.1
rs3180	Whole blood_ENSG00000107	20	0.130843	1.710	0.028009	0.778317	C10orf54	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05831	1.672369	ENSG00000107738.15
rs3180	Thyroid_ENSG00000107742.8	20	0.056016	-5.050	0.028104	2.2999	SPOCK2	Thyroid	GTEEx_v6	T	C	73762673	10	rs2219837	0.172212	1.667053	ENSG00000107742.8
rs7814941	Brain cerebellar hemisphere_	18	0.444142	-3.547	0.028369	1.618206	FAM49B	Brain cere	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.1575	1.593162	ENSG00000153310.14
rs7814941	Muscle skeletal_ENSG000001	20	0.024889	-2.535	0.030042	1.168661	CHST3	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	0.086459	1.636988	ENSG00000122863.5
rs7814941	Liver_ENSG00000153310.14	17	0.357777	4.874	0.030539	2.253214	FAM49B	Liver	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.216395	1.564207	ENSG00000153310.14
rs3180	Spleen_ENSG00000166228.4	2	NA	11.784	0.031013	5.463436	PCBD1	Spleen	GTEEx_v6	C	T	73646408	10	rs1437267	0.258072	2.054766	ENSG00000166228.4
rs3180	Adrenal gland_ENSG0000022	5	0.511636	14.737	0.031282	6.843299	SNORA11	Adrenal gli	GTEEx_v6	C	T	73899093	10	rs1245515	-0.27411	1.960011	ENSG00000221164.1
rs7814941	Skin not sun exposed suprapu	20	0.00123	2.916	0.033297	1.369774	GSDMC	Skin not su	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.12945	1.547534	ENSG00000147697.4
rs3180	Testis_ENSG00000148719.10	20	0.14654	5.155	0.033414	2.423485	DNAJB12	Testis	GTEEx_v6	T	C	73762673	10	rs2219837	-0.17578	1.563507	ENSG00000148719.10
rs3180	Uterus_ENSG00000107742.8	20	0.286874	9.144	0.033677	4.305229	SPOCK2	Uterus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.31181	1.51802	ENSG00000107742.8
rs7814941	Muscle skeletal_ENSG000002	20	0.468036	3.869	0.033691	1.821964	RP11-473C	Muscle ske	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.171801	1.552856	ENSG00000254317.1
rs7814941	Colon sigmoid_ENSG0000015	17	0.494695	4.876	0.033776	2.29691	ASAP1	Colon sigm	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.216482	1.528548	ENSG00000153317.10
rs3180	Small intestine terminal ileum	20	0.003551	4.674	0.034246	2.20767	ANAPC16	Small intest	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15938	1.517414	ENSG00000166295.4
rs3180	Testis_ENSG00000166295.4	20	0.573613	3.794	0.0353	1.802464	ANAPC16	Testis	GTEEx_v6	T	C	73762673	10	rs2219837	-0.12938	1.536031	ENSG00000166295.4
rs3180	Brain cerebellar hemisphere_	20	0.030269	-6.888	0.035437	3.27458	SPOCK2	Brain cere	GTEEx_v6	T	C	73762673	10	rs2219837	0.234864	1.51175	ENSG00000107742.8
rs3180	Breast mammary tissue_ENSG	20	0.078392	4.615	0.035846	2.199175	CDH23	Breast mai	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15738	1.533192	ENSG00000107736.15
rs3180	Pituitary_ENSG00000200356.:	1	NA	-23.399	0.037535	11.25028	RNU6-833l	Pituitary	GTEEx_v6	C	G	74046191	10	rs1074039	-0.39077	2.005332	ENSG00000200356.1
rs3180	Skin sun exposed lower leg_EI	20	0.773167	2.589	0.038389	1.250175	MICU1	Skin sun e	GTEEx_v6	T	C	73762673	10	rs2219837	-0.08827	1.508692	ENSG00000107745.12
rs3180	Nerve tibial_ENSG0000016820	20	0.723274	-3.629	0.039877	1.76592	DDIT4	Nerve tibi	GTEEx_v6	T	C	73762673	10	rs2219837	0.123749	1.48677	ENSG00000168209.4
rs12310519	Prostate_ENSG00000134532.:	11	0.101047	5.523	0.040299	2.69345	SOX5	Prostate	GTEEx_v6	C	T	23982559	12	rs9804988	-0.3198	1.419583	ENSG00000134532.11

rs3180	Skin not sun exposed suprapu	20	0.956216	-4.499	0.041132	2.203198 SPOCK2	Skin not su GTEX_v6	T	C	73762673	10 rs2219837	0.153428	1.466096	ENSG00000107742.8
rs3180	Artery coronary_ENSG000001	20	0.695018	-5.698	0.041227	2.791511 DNAJB12	Artery coro GTEX_v6	T	C	73762673	10 rs2219837	0.194307	1.452303	ENSG00000148719.10
rs3180	Esophagus mucosa_ENSG0000	20	0.12547	-3.793	0.043603	1.879542 UNC5B	Esophagus GTEX_v6	T	C	73762673	10 rs2219837	0.129331	1.441153	ENSG00000107731.8
rs7814941	Cells transformed fibroblasts_	20	0.445671	-2.202	0.044053	1.09336 ASAP1	Cells trans GTEX_v6	A	G	1.31E+08	8 rs1095648	-0.09775	1.417657	ENSG00000153317.10
rs3180	Cells EBV-transformed lympho	20	0.912572	7.253	0.044475	3.609149 SPOCK2	Cells EBV-t GTEX_v6	T	C	73762673	10 rs2219837	-0.24732	1.41392	ENSG00000107742.8
rs3180	Brain caudate basal ganglia_E	2	NA	9.632	0.045307	4.811914 PCBD1	Brain caud GTEX_v6	C	T	73646408	10 rs1437267	0.210951	1.738958	ENSG00000166228.4
rs12310519	Brain frontal cortex BA9_ENS	11	0.027978	-6.871	0.045944	3.442574 RP11-444C	Brain front GTEX_v6	C	T	23982559	12 rs9804988	0.397835	1.362063	ENSG00000255864.1
rs3180	Adipose subcutaneous_ENSG0	5	0.020308	-11.157	0.046035	5.592164 SNORA11	Adipose su GTEX_v6	C	T	73899093	10 rs1245515	0.207516	1.683327	ENSG00000221164.1
rs3180	Liver_ENSG00000138286.10	1	NA	-12.334	0.046986	6.209311 FAM149B1	Liver GTEX_v6	C	G	74046191	10 rs1074039	-0.20598	1.802799	ENSG00000138286.10
rs3180	Brain nucleus accumbens basi	20	0.188753	-7.468	0.047262	3.764301 MICU1	Brain nuck GTEX_v6	T	C	73762673	10 rs2219837	0.254664	1.375647	ENSG00000107745.12
rs3180	Uterus_ENSG00000138303.13	20	0.535457	-6.985	0.047626	3.526769 ASCC1	Uterus GTEX_v6	T	C	73762673	10 rs2219837	0.238203	1.355343	ENSG00000138303.13
rs3180	Stomach_ENSG00000198246.	20	0.611983	4.272	0.047962	2.160043 SLC29A3	Stomach GTEX_v6	T	C	73762673	10 rs2219837	-0.14567	1.386354	ENSG00000198246.7
rs3180	Testis_ENSG00000107745.12	20	0.141908	-4.306	0.048823	2.185672 MICU1	Testis GTEX_v6	T	C	73762673	10 rs2219837	0.146837	1.375584	ENSG00000107745.12
rs3180	Artery tibial_ENSG000001487	20	0.579466	2.458	0.049361	1.250584 DNAJB12	Artery tibi GTEX_v6	T	C	73762673	10 rs2219837	-0.08382	1.381437	ENSG00000148719.10
rs3180	Esophagus gastroesophageal_j	20	0.560924	3.710	0.049794	1.89104 PSAP	Esophagus GTEX_v6	T	C	73762673	10 rs2219837	-0.1265	1.362597	ENSG00000197746.9
rs3180	Small intestine terminal ileum	20	0.289478	3.976	0.049828	2.026909 CHST3	Small intes GTEX_v6	T	C	73762673	10 rs2219837	-0.13557	1.339885	ENSG00000122863.5
rs3180	Colon sigmoid_ENSG0000012	1	NA	-13.247	0.050075	6.761014 ECD	Colon signr GTEX_v6	C	G	74046191	10 rs1074039	-0.22123	1.761467	ENSG00000122882.6
rs3180	Pituitary_ENSG00000166295.	20	0.176831	-4.868	0.050523	2.489129 ANAPC16	Pituitary GTEX_v6	T	C	73762673	10 rs2219837	0.165982	1.340427	ENSG00000166295.4
rs3180	Artery coronary_ENSG000002	1	NA	-15.242	0.050662	7.798889 DNAJC9	Artery cori GTEX_v6	C	G	74046191	10 rs1074039	-0.25454	1.748131	ENSG00000213551.4
rs3180	Ovary_ENSG00000138303.13	20	0.351928	-6.965	0.050743	3.565154 ASCC1	Ovary GTEX_v6	T	C	73762673	10 rs2219837	0.237508	1.337755	ENSG00000138303.13
rs3180	Skin not sun exposed suprapu	20	0.0014	-4.025	0.050789	2.060738 ASCC1	Skin not su GTEX_v6	T	C	73762673	10 rs2219837	0.137258	1.361459	ENSG00000138303.13
rs7814941	Muscle skeletal_ENSG000001	20	0.35191	1.999	0.051561	1.026934 ASAP1	Muscle ske GTEX_v6	A	G	1.31E+08	8 rs1095648	0.088765	1.344765	ENSG00000153317.10
rs3180	Colon sigmoid_ENSG0000012	8	0.471312	7.987	0.051623	4.103652 P4HA1	Colon signr GTEX_v6	T	C	73858549	10 rs1668156	-0.14935	1.571648	ENSG00000122884.8
rs7814941	Brain caudate basal ganglia_E	18	0.863744	-3.660	0.052139	1.8846 ASAP1	Brain caud GTEX_v6	A	G	1.31E+08	8 rs1095648	-0.1625	1.315159	ENSG00000153317.10
rs7814941	Small intestine terminal ileum	16	0.163804	-10.848	0.052899	5.604135 RP11-473C	Small intes GTEX_v6	A	G	1.31E+08	8 rs1095648	-0.48166	1.295654	ENSG00000254263.1
rs3180	Brain nucleus accumbens basi	1	NA	-11.982	0.053231	6.198294 MRPS16	Brain nuck GTEX_v6	C	G	74046191	10 rs1074039	-0.20009	1.688471	ENSG00000182180.9
rs3180	Liver_ENSG00000107738.15	20	0.234346	3.947	0.053553	2.044592 C10orf54	Liver GTEX_v6	T	C	73762673	10 rs2219837	-0.13459	1.31781	ENSG00000107738.15
rs3180	Brain cerebellar hemisphere_	20	0.221696	9.401	0.054085	4.88067 UNC5B-AS	Brain cerel GTEX_v6	T	C	73762673	10 rs2219837	-0.32057	1.309234	ENSG00000237512.2
rs3180	Skin not sun exposed suprapu	2	NA	-6.658	0.054355	3.460613 PCBD1	Skin not su GTEX_v6	C	T	73646408	10 rs1437267	-0.14582	1.619693	ENSG00000166228.4
rs3180	Artery tibial_ENSG000002211	5	0.198967	-10.718	0.054392	5.571678 SNORA11	Artery tibi GTEX_v6	C	T	73899093	10 rs1245515	0.199359	1.558864	ENSG00000221164.1
rs7814941	Whole blood_ENSG000001471	20	0.398832	3.909	0.054706	2.034791 GSDMC	Whole blo GTEX_v6	A	G	1.31E+08	8 rs1095648	0.173571	1.315573	ENSG00000147697.4
rs3180	Vagina_ENSG00000122863.5	20	0.972245	5.737	0.055438	2.995169 CHST3	Vagina GTEX_v6	T	C	73762673	10 rs2219837	-0.19563	1.292069	ENSG00000122863.5
rs7814941	Skin sun exposed lower leg_EI	20	0.145208	2.024	0.056521	1.061233 FAM49B	Skin sun e GTEX_v6	A	G	1.31E+08	8 rs1095648	0.089855	1.298747	ENSG00000153310.14
rs3180	Artery aorta_ENSG000001982	20	0.763849	4.047	0.057093	2.127127 SLC29A3	Artery aor GTEX_v6	T	C	73762673	10 rs2219837	-0.13801	1.304075	ENSG00000198246.7
rs3180	Brain nucleus accumbens basi	20	0.871299	-4.087	0.058198	2.157813 ANAPC16	Brain nuck GTEX_v6	T	C	73762673	10 rs2219837	0.139378	1.276445	ENSG00000166295.4
rs3180	Thyroid_ENSG00000197746.9	20	0.287943	2.380	0.059548	1.263216 PSAP	Thyroid GTEX_v6	T	C	73762673	10 rs2219837	-0.08116	1.288198	ENSG00000197746.9
rs3180	Nerve tibial_ENSG000001383	20	0.233245	2.334	0.059738	1.239924 ASCC1	Nerve tibi GTEX_v6	T	C	73762673	10 rs2219837	-0.0796	1.285602	ENSG00000138303.13
rs3180	Colon transverse_ENSG0000	20	0.568526	4.368	0.06107	2.332041 DDT14	Colon tran GTEX_v6	T	C	73762673	10 rs2219837	-0.14895	1.26816	ENSG00000168209.4
rs12310519	Esophagus mucosa_ENSG0000	11	0.772613	4.146	0.061177	2.214326 RP11-444C	Esophagus GTEX_v6	C	T	23982559	12 rs9804988	-0.24004	1.251922	ENSG00000255864.1
rs3180	Colon sigmoid_ENSG0000010	20	0.027215	5.482	0.062019	2.937562 C10orf54	Colon signr GTEX_v6	T	C	73762673	10 rs2219837	-0.18694	1.255719	ENSG00000107738.15
rs7814941	Vagina_ENSG00000224110.3	17	0.278475	4.699	0.063597	2.53338 RP11-274A	Vagina GTEX_v6	A	G	1.31E+08	8 rs1095648	0.208654	1.214033	ENSG00000224110.3
rs3180	Adipose visceral omentum_EI	5	0.50952	9.552	0.063986	5.156916 RP11-152A	Adipose vi GTEX_v6	C	T	73899093	10 rs1245515	-0.17767	1.435976	ENSG00000272599.1
rs3180	Thyroid_ENSG00000221164.1	5	0.720004	-10.102	0.064089	5.456201 SNORA11	Thyroid GTEX_v6	C	T	73899093	10 rs1245515	0.187906	1.442393	ENSG00000221164.1
rs3180	Muscle skeletal_ENSG000002	1	NA	-9.453	0.064123	5.106237 DNAJC9-A'	Muscle ske GTEX_v6	C	G	74046191	10 rs1074039	-0.15787	1.571397	ENSG00000236756.4
rs3180	Artery tibial_ENSG000001228	8	0.015306	-3.851	0.064312	2.081587 P4HA1	Artery tibi GTEX_v6	T	C	73858549	10 rs1668156	0.072013	1.436871	ENSG00000122884.8
rs3180	Brain cerebellum_ENSG0000	20	0.071013	-4.709	0.064648	2.548629 CHST3	Brain cerel GTEX_v6	T	C	73762673	10 rs2219837	0.160579	1.23038	ENSG00000122863.5
rs3180	Esophagus mucosa_ENSG0000	20	0.773886	3.100	0.0647	1.677988 PSAP	Esophagus GTEX_v6	T	C	73762673	10 rs2219837	-0.1057	1.246	ENSG00000197746.9
rs3180	Brain cerebellar hemisphere_	20	0.3177	-6.152	0.065084	3.33526 CHST3	Brain cerel GTEX_v6	T	C	73762673	10 rs2219837	0.2098	1.221793	ENSG00000122863.5
rs3180	Skin not sun exposed suprapu	5	0.696711	-9.322	0.065459	5.060411 RP11-152A	Skin not su GTEX_v6	C	T	73899093	10 rs1245515	0.173386	1.421802	ENSG00000272599.1
rs3180	Ovary_ENSG00000272630.1	8	0.284741	-14.093	0.066236	7.672623 RP11-344A	Ovary GTEX_v6	T	C	73865131	10 rs1100017	0.262134	1.387602	ENSG00000272630.1

rs3180	Artery tibial_ENSG000002137	16	0.705801	2.598	0.067335	1.419889	RPL17P50	Artery tibi; GTEx_v6	A	G	73820622	10	rs3180	-0.0865	1.228618	ENSG00000213700.3
rs3180	Esophagus muscularis_ENSG0	2	NA	5.749	0.067623	3.145557	PCBD1	Esophagus GTEx_v6	C	T	73646408	10	rs1437267	0.125893	1.454714	ENSG00000166228.4
rs3180	Skin not sun exposed suprapu	20	0.020196	-3.008	0.067831	1.647221	ANAPC16	Skin not su GTEx_v6	T	C	73762673	10	rs2219837	0.102574	1.220052	ENSG00000166295.4
rs3180	Brain cerebellum_ENSG00000	20	0.038701	-5.546	0.068041	3.039574	SPOCK2	Brain cerel GTEx_v6	T	C	73762673	10	rs2219837	0.189133	1.206119	ENSG00000107742.8
rs7814941	Artery aorta_ENSG000001533	20	0.163053	1.402	0.068247	0.76894	FAM49B	Artery aor; GTEx_v6	A	G	1.31E+08	8	rs1095648	0.062252	1.203782	ENSG00000153310.14
rs3180	Skin sun exposed lower leg_EI	1	NA	8.040	0.06825	4.409662	RP11-152N	Skin sun e; GTEx_v6	C	G	74046191	10	rs1074039	0.134274	1.516588	ENSG00000227540.1
rs3180	Brain anterior cingulate corte	20	0.162279	-5.430	0.068302	2.9785	PSAP	Brain ante GTEx_v6	T	C	73762673	10	rs2219837	0.185157	1.189074	ENSG00000197746.9
rs3180	Breast mammary tissue_ENSG	20	0.127107	-5.360	0.068336	2.940357	SPOCK2	Breast mai GTEx_v6	T	C	73762673	10	rs2219837	0.182764	1.215299	ENSG00000107742.8
rs7814941	Lung_ENSG00000243402.1	20	0.380092	4.226	0.068448	2.319575	RP11-473C	Lung GTEx_v6	A	G	1.31E+08	8	rs1095648	0.187651	1.206476	ENSG00000243402.1
rs12310519	Brain cerebellum_ENSG00000	11	0.424484	-2.601	0.069106	1.430833	SOX5	Brain cerel GTEx_v6	C	T	23982559	12	rs9804988	0.15059	1.180138	ENSG00000134532.11
rs3180	Heart left ventricle_ENSG0000	20	0.336765	-2.488	0.069222	1.369255	ANAPC16	Heart left \ GTEx_v6	T	C	73762673	10	rs2219837	0.084837	1.209711	ENSG00000166295.4
rs3180	Brain cerebellum_ENSG00000	2	NA	9.588	0.069626	5.284715	PCBD1	Brain cerel GTEx_v6	C	T	73646408	10	rs1437267	0.209983	1.413342	ENSG00000166228.4
rs3180	Testis_ENSG00000138286.10	1	NA	10.609	0.069835	5.851529	FAM149B1	Testis GTEx_v6	C	G	74046191	10	rs1074039	0.177165	1.48347	ENSG00000138286.10
rs3180	Brain cerebellum_ENSG00000	20	0.021861	-7.766	0.070089	4.287361	UNC5B-AS	Brain cerel GTEx_v6	T	C	73762673	10	rs2219837	0.264815	1.192067	ENSG00000237512.2
rs3180	Nerve tibial_ENSG000001077	20	0.232507	-3.880	0.070118	2.142097	SPOCK2	Nerve tibia; GTEx_v6	T	C	73762673	10	rs2219837	0.132296	1.207286	ENSG00000107742.8
rs3180	Esophagus muscularis_ENSG0	20	0.572491	4.028	0.070245	2.225098	UNC5B-AS	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	-0.13736	1.204676	ENSG00000237512.2
rs3180	Spleen_ENSG00000138303.13	20	0.890238	-5.681	0.071121	3.147866	ASCC1	Spleen GTEx_v6	T	C	73762673	10	rs2219837	0.193721	1.180146	ENSG00000138303.13
rs12310519	Liver_ENSG00000134532.11	11	0.458107	-5.164	0.071308	2.863491	SOX5	Liver GTEx_v6	C	T	23982559	12	rs9804988	0.299015	1.163998	ENSG00000134532.11
rs3180	Brain cerebellar hemisphere_	20	0.569459	-10.396	0.071675	5.771894	NPM1P24	Brain cerel GTEx_v6	T	C	73762673	10	rs2219837	0.35451	1.176514	ENSG00000215086.2
rs3180	Pituitary_ENSG00000200170.	20	0.072816	-9.607	0.072304	5.345461	Y_RNA	Pituitary GTEx_v6	T	C	73762673	10	rs2219837	0.327594	1.171548	ENSG00000200170.1
rs3180	Brain hippocampus_ENSG000	20	0.67774	-5.630	0.07251	3.135107	C10orf105	Brain hipp GTEx_v6	T	C	73762673	10	rs2219837	0.191995	1.167264	ENSG00000214688.4
rs3180	Esophagus muscularis_ENSG0	20	0.18109	-2.872	0.074203	1.608764	CHST3	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	0.097943	1.178141	ENSG00000122863.5
rs3180	Brain anterior cingulate corte	20	0.001588	-6.290	0.075216	3.535526	C10orf105	Brain ante GTEx_v6	T	C	73762673	10	rs2219837	0.214496	1.144706	ENSG00000214688.4
rs3180	Adipose subcutaneous_ENSG0	20	0.069395	-3.918	0.075274	2.202625	C10orf54	Adipose su GTEx_v6	T	C	73762673	10	rs2219837	0.133604	1.174314	ENSG00000107738.15
rs7814941	Heart atrial appendage_ENSG	19	0.002536	4.611	0.076352	2.602003	GSDMC	Heart atria GTEx_v6	A	G	1.31E+08	8	rs1095648	0.204747	1.147447	ENSG00000147697.4
rs3180	Spleen_ENSG00000221164.1	5	0.285236	16.805	0.076406	9.483796	SNORA11	Spleen GTEx_v6	C	T	73899093	10	rs1245515	-0.31257	1.297581	ENSG00000221164.1
rs3180	Artery coronary_ENSG000001	20	0.045118	7.126	0.077408	4.035368	OIT3	Artery cori GTEx_v6	T	C	73762673	10	rs2219837	-0.243	1.148696	ENSG00000138315.8
rs3180	Liver_ENSG00000197746.9	20	0.696858	-4.089	0.079053	2.328417	PSAP	Liver GTEx_v6	T	C	73762673	10	rs2219837	0.139441	1.133534	ENSG00000197746.9
rs3180	Adrenal gland_ENSG00000168	20	0.701775	5.782	0.079173	3.29349	DDIT4	Adrenal gl; GTEx_v6	T	C	73762673	10	rs2219837	-0.19716	1.139457	ENSG00000168209.4
rs3180	Skin not sun exposed suprapu	20	0.933606	3.748	0.079502	2.137288	UNC5B-AS	Skin not su GTEx_v6	T	C	73762673	10	rs2219837	-0.1278	1.143482	ENSG00000237512.2
rs3180	Brain cerebellum_ENSG00000	20	0.625605	9.119	0.079628	5.202148	Y_RNA	Brain cerel GTEx_v6	T	C	73762673	10	rs2219837	-0.31094	1.131886	ENSG00000200170.1
rs3180	Esophagus mucosa_ENSG0000	20	0.169662	-5.396	0.080144	3.083768	Y_RNA	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	0.184008	1.142123	ENSG00000200170.1
rs3180	Brain nucleus accumbens bas	8	0.102753	12.007	0.080193	6.862765	RP11-344N	Brain nuck GTEx_v6	T	C	73865131	10	rs1100017	-0.22333	1.26901	ENSG00000272630.1
rs3180	Skin not sun exposed suprapu	20	0.801379	-4.448	0.080307	2.543406	CDH23	Skin not su GTEx_v6	T	C	73762673	10	rs2219837	0.151683	1.13865	ENSG00000107736.15
rs7814941	Brain hippocampus_ENSG000	17	0.024705	-6.608	0.080787	3.784094	GSDMC	Brain hipp GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.29338	1.106213	ENSG00000147697.4
rs12310519	Testis_ENSG00000256321.1	11	0.119139	4.639	0.08098	2.658648	RP11-153K	Testis GTEx_v6	C	T	23982559	12	rs9804988	-0.26862	1.115021	ENSG00000256321.1
rs3180	Skin sun exposed lower leg_EI	1	NA	5.147	0.0817	2.956515	FAM149B1	Skin sun e; GTEx_v6	C	G	74046191	10	rs1074039	0.085955	1.372963	ENSG00000138286.10
rs3180	Colon transverse_ENSG00000	20	0.429675	3.286	0.082236	1.891042	SPOCK2	Colon tran GTEx_v6	T	C	73762673	10	rs2219837	-0.11207	1.125013	ENSG00000107742.8
rs3180	Artery tibial_ENSG000001228	1	NA	-4.577	0.082617	2.636698	ECD	Artery tibi; GTEx_v6	C	G	74046191	10	rs1074039	-0.07643	1.363653	ENSG00000122882.6
rs3180	Pituitary_ENSG00000182180.	1	NA	-12.633	0.084255	7.316783	MRPS16	Pituitary GTEx_v6	C	G	74046191	10	rs1074039	-0.21096	1.320183	ENSG00000182180.9
rs3180	Colon sigmoid_ENSG0000016	20	0.124645	-5.060	0.084794	2.935988	DDIT4	Colon signr GTEx_v6	T	C	73762673	10	rs2219837	0.172554	1.106633	ENSG00000168209.4
rs3180	Heart left ventricle_ENSG000	20	0.463257	4.566	0.085379	2.654031	SLC29A3	Heart left \ GTEx_v6	T	C	73762673	10	rs2219837	-0.15569	1.108901	ENSG00000198246.7
rs3180	Colon sigmoid_ENSG0000013	1	NA	7.563	0.085653	4.4004	FAM149B1	Colon signr GTEx_v6	C	G	74046191	10	rs1074039	0.126308	1.321866	ENSG00000138286.10
rs3180	Colon transverse_ENSG00000	20	0.099872	-4.536	0.087331	2.653183	SLC29A3	Colon tran GTEx_v6	T	C	73762673	10	rs2219837	0.154678	1.096392	ENSG00000198246.7
rs3180	Adipose subcutaneous_ENSG0	20	0.095336	2.455	0.088986	1.443602	SLC29A3	Adipose su GTEx_v6	T	C	73762673	10	rs2219837	-0.08372	1.09348	ENSG00000198246.7
rs3180	Small intestine terminal ileum	20	0.038958	6.353	0.089525	3.741454	RP11-150C	Small intes GTEx_v6	T	C	73762673	10	rs2219837	-0.21663	1.067766	ENSG00000272988.1
rs7814941	Esophagus gastroesophageal j	19	0.585657	-4.855	0.090394	2.866916	GSDMC	Esophagus GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.21555	1.066976	ENSG00000147697.4
rs7814941	Skin sun exposed lower leg_EI	20	0.030259	-3.627	0.091498	2.149528	RP11-419K	Skin sun e; GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.16106	1.070231	ENSG00000254223.1
rs3180	Brain nucleus accumbens bas	20	0.218556	-7.319	0.091982	4.343772	UNC5B-AS	Brain nuck GTEx_v6	T	C	73762673	10	rs2219837	0.249592	1.061602	ENSG00000237512.2
rs3180	Pituitary_ENSG00000198246.	20	0.605927	6.749	0.092432	4.01056	SLC29A3	Pituitary GTEx_v6	T	C	73762673	10	rs2219837	-0.23013	1.057348	ENSG00000198246.7

rs3180	Artery tibial_ENSG000002367	1 NA	9.381	0.09292	5.583473	DNAJC9-A ^t	Artery tibi; GTEx_v6	C	G	74046191	10 rs1074039	0.156668	1.275403	ENSG00000236756.4
rs3180	Brain cerebellar hemisphere_	16 0.401207	-5.636	0.093142	3.356424	RPL17P50	Brain cerel GTEx_v6	A	G	73820622	10 rs3180	0.187666	1.054813	ENSG00000213700.3
rs7814941	Artery aorta_ENSG000001533	20 0.296169	2.342	0.093379	1.39601	ASAP1	Artery aor; GTEx_v6	A	G	1.31E+08	8 rs1095648	0.103997	1.056998	ENSG00000153317.10
rs3180	Vagina_ENSG00000272630.1	8 0.250063	-15.743	0.094676	9.420063	RP11-344N	Vagina GTEx_v6	T	C	73865131	10 rs1100017	0.292822	1.16074	ENSG00000272630.1
rs3180	Heart atrial appendage_ENSG	20 0.940358	-3.379	0.094996	2.024071	MICU1	Heart atria GTEx_v6	T	C	73762673	10 rs2219837	0.115238	1.055538	ENSG00000107745.12
rs3180	Prostate_ENSG00000168209.	20 0.426988	7.726	0.095215	4.630391	DDIT4	Prostate GTEx_v6	T	C	73762673	10 rs2219837	-0.26345	1.043984	ENSG00000168209.4
rs3180	Cells transformed fibroblasts_	20 0.451139	1.918	0.095353	1.15	MICU1	Cells trans GTEx_v6	T	C	73762673	10 rs2219837	-0.0654	1.059658	ENSG00000107745.12
rs3180	Testis_ENSG00000272627.1	20 0.373432	-6.250	0.096127	3.756039	RP11-354E	Testis GTEx_v6	T	C	73762673	10 rs2219837	0.213117	1.04984	ENSG00000272627.1
rs3180	Liver_ENSG00000122882.6	1 NA	11.375	0.097324	6.860581	ECD	Liver GTEx_v6	C	G	74046191	10 rs1074039	0.189956	1.222055	ENSG00000122882.6
rs7814941	Thyroid_ENSG00000254263.1	20 0.740451	3.544	0.098293	2.143961	RP11-473C	Thyroid GTEx_v6	A	G	1.31E+08	8 rs1095648	0.15737	1.036127	ENSG00000254263.1
rs3180	Ovary_ENSG00000156026.10	20 0.276015	5.585	0.098531	3.380441	MCU	Ovary GTEx_v6	T	C	73762673	10 rs2219837	-0.19043	1.027487	ENSG00000156026.10
rs3180	Pituitary_ENSG00000213551.	1 NA	-12.435	0.09877	7.532703	DNAJC9	Pituitary GTEx_v6	C	G	74046191	10 rs1074039	-0.20767	1.2076	ENSG00000213551.4
rs3180	Brain hippocampus_ENSG000	5 0.164994	-16.524	0.100183	10.05157	RP11-152A	Brain hippoc GTEx_v6	C	T	73899093	10 rs1245515	0.307355	1.127613	ENSG00000272599.1
rs3180	Skin not sun exposed suprapu	20 0.919969	2.404	0.10082	1.464932	PSAP	Skin not su GTEx_v6	T	C	73762673	10 rs2219837	-0.08197	1.030229	ENSG00000197746.9
rs3180	Stomach_ENSG00000272627.	20 0.810605	5.207	0.101139	3.176248	RP11-354E	Stomach GTEx_v6	T	C	73762673	10 rs2219837	-0.17756	1.026966	ENSG00000272627.1
rs3180	Brain putamen basal ganglia_	20 0.548427	-5.810	0.102211	3.555284	ANAPC16	Brain puta GTEx_v6	T	C	73762673	10 rs2219837	0.198126	1.00915	ENSG00000166295.4
rs3180	Pancreas_ENSG00000138286.	1 NA	7.881	0.102238	4.822851	FAM149B1	Pancreas GTEx_v6	C	G	74046191	10 rs1074039	0.131613	1.196648	ENSG00000138286.10
rs3180	Brain putamen basal ganglia_	20 0.387614	7.949	0.10262	4.869597	CDH23	Brain puta GTEx_v6	T	C	73762673	10 rs2219837	-0.27105	1.007325	ENSG00000107736.15
rs3180	Small intestine terminal ileum	20 0.031484	4.497	0.102916	2.757665	DNAJB12	Small intes GTEx_v6	T	C	73762673	10 rs2219837	-0.15336	1.003922	ENSG00000148719.10
rs3180	Brain anterior cingulate cort:	20 0.094533	7.569	0.103035	4.642928	DNAJB12	Brain ante GTEx_v6	T	C	73762673	10 rs2219837	-0.25812	1.000927	ENSG00000148719.10
rs3180	Skin sun exposed lower leg_EI	1 NA	-5.848	0.104187	3.598985	DNAJC9	Skin sun ex GTEx_v6	C	G	74046191	10 rs1074039	-0.09766	1.193534	ENSG00000213551.4
rs3180	Nerve tibial_ENSG000001077	20 0.392965	2.016	0.105125	1.244127	MICU1	Nerve tibia; GTEx_v6	T	C	73762673	10 rs2219837	-0.06875	1.012709	ENSG00000107745.12
rs3180	Brain nucleus accumbens bas:	20 0.170975	-4.664	0.105888	2.884375	UNC5B	Brain nuck GTEx_v6	T	C	73762673	10 rs2219837	0.159039	0.996402	ENSG00000107731.8
rs3180	Heart left ventricle_ENSG000	20 0.863247	3.485	0.106674	2.159925	MCU	Heart left \ GTEx_v6	T	C	73762673	10 rs2219837	-0.11883	1.003215	ENSG00000156026.10
rs3180	Muscle skeletal_ENSG0000001	2 NA	-3.746	0.107516	2.327755	PCBD1	Muscle ske GTEx_v6	C	T	73646408	10 rs1437267	-0.08205	1.13833	ENSG00000166228.4
rs3180	Stomach_ENSG00000227382.	1 NA	-12.686	0.108618	7.906601	EIF4A2P2	Stomach GTEx_v6	C	G	74046191	10 rs1074039	-0.21185	1.157449	ENSG00000227382.1
rs3180	Esophagus gastroesophageal	5 0.10702	-11.256	0.108637	7.015799	RP11-152A	Esophagus GTEx_v6	C	T	73899093	10 rs1245515	0.209358	1.092098	ENSG00000272599.1
rs3180	Lung_ENSG00000215086.2	20 0.183672	-4.149	0.108899	2.588051	NPM1P24	Lung GTEx_v6	T	C	73762673	10 rs2219837	0.141483	0.996578	ENSG00000215086.2
rs3180	Artery aorta_ENSG000002146	20 0.165278	5.577	0.109382	3.483341	C10orf105	Artery aor; GTEx_v6	T	C	73762673	10 rs2219837	-0.19017	0.991779	ENSG00000214688.4
rs3180	Uterus_ENSG00000213700.3	16 0.452032	-4.572	0.109922	2.859869	RPL17P50	Uterus GTEx_v6	A	G	73820622	10 rs3180	0.152235	0.97127	ENSG00000213700.3
rs12310519	Brain hippocampus_ENSG000	11 0.15888	-3.137	0.110111	1.963453	SOX5	Brain hippo GTEx_v6	C	T	23982559	12 rs9804988	0.181632	0.963463	ENSG00000134532.11
rs7814941	Esophagus muscularis_ENSG0	20 0.638969	-3.588	0.110191	2.245987	GSDMC	Esophagus GTEx_v6	A	G	1.31E+08	8 rs1095648	-0.15929	0.981241	ENSG00000147697.4
rs3180	Brain frontal cortex BA9_ENS	20 0.271686	-2.777	0.110389	1.739549	CHST3	Brain front GTEx_v6	T	C	73762673	10 rs2219837	0.094699	0.976941	ENSG00000122863.5
rs7814941	Spleen_ENSG00000224110.3	17 0.000975	7.042	0.111138	4.420258	RP11-274A	Spleen GTEx_v6	A	G	1.31E+08	8 rs1095648	0.312661	0.965271	ENSG00000224110.3
rs3180	Cells transformed fibroblasts_	5 0.049923	-6.565	0.112014	4.13099	SNORA11	Cells trans GTEx_v6	C	T	73899093	10 rs1245515	0.122109	1.082188	ENSG00000221164.1
rs3180	Heart left ventricle_ENSG000	1 NA	-8.394	0.112091	5.283173	RP11-152A	Heart left \ GTEx_v6	C	G	74046191	10 rs1074039	-0.14018	1.137687	ENSG00000227540.1
rs12310519	Artery coronary_ENSG000002	11 0.142729	3.803	0.112525	2.396736	RP11-444C	Artery cor; GTEx_v6	C	T	23982559	12 rs9804988	-0.22022	0.961921	ENSG00000255864.1
rs3180	Prostate_ENSG00000166228.	2 NA	-11.676	0.113391	7.375179	PCBD1	Prostate GTEx_v6	C	T	73646408	10 rs1437267	-0.2557	1.08419	ENSG00000166228.4
rs3180	Prostate_ENSG00000122863.	20 0.40637	4.239	0.114954	2.689115	CHST3	Prostate GTEx_v6	T	C	73762673	10 rs2219837	-0.14455	0.95722	ENSG00000122863.5
rs3180	Prostate_ENSG00000107736.	20 0.00757	5.801	0.115306	3.683376	CDH23	Prostate GTEx_v6	T	C	73762673	10 rs2219837	-0.1978	0.955821	ENSG00000107736.15
rs7814941	Pancreas_ENSG00000153310.	20 0.37777	-2.343	0.116101	1.491287	FAM49B	Pancreas GTEx_v6	A	G	1.31E+08	8 rs1095648	-0.10404	0.952889	ENSG00000153310.14
rs3180	Brain nucleus accumbens bas:	20 0.253423	-6.106	0.116221	3.887303	MCU	Brain nuck GTEx_v6	T	C	73762673	10 rs2219837	0.208225	0.953497	ENSG00000156026.10
rs3180	Artery coronary_ENSG0000001	20 0.424687	4.049	0.116494	2.579558	C10orf54	Artery cor; GTEx_v6	T	C	73762673	10 rs2219837	-0.13807	0.95694	ENSG00000107738.15
rs3180	Esophagus muscularis_ENSG0	8 0.230224	-8.269	0.116838	5.272889	RP11-344A	Esophagus GTEx_v6	T	C	73865131	10 rs1100017	0.153801	0.1055138	ENSG00000272630.1
rs3180	Pituitary_ENSG00000214688.	20 0.016794	-8.032	0.117246	5.127836	C10orf105	Pituitary GTEx_v6	T	C	73762673	10 rs2219837	0.273906	0.947883	ENSG00000214688.4
rs3180	Skin not sun exposed suprapu	20 0.03672	3.393	0.117267	2.166213	SLC29A3	Skin not su GTEx_v6	T	C	73762673	10 rs2219837	-0.1157	0.958971	ENSG00000198246.7
rs3180	Brain putamen basal ganglia_	20 0.217396	-5.059	0.117973	3.235873	MICU1	Brain puta GTEx_v6	T	C	73762673	10 rs2219837	0.172504	0.943518	ENSG00000107745.12
rs7814941	Brain hippocampus_ENSG000	17 0.014529	5.988	0.118446	3.835289	RP11-473C	Brain hippo GTEx_v6	A	G	1.31E+08	8 rs1095648	0.265874	0.934222	ENSG00000253720.1
rs3180	Pancreas_ENSG00000221164.	5 0.18063	10.977	0.118924	7.039624	SNORA11	Pancreas GTEx_v6	C	T	73899093	10 rs1245515	-0.20417	1.039592	ENSG00000221164.1
rs3180	Pituitary_ENSG00000197746.	20 0.004477	-5.370	0.119383	3.447824	PSAP	Pituitary GTEx_v6	T	C	73762673	10 rs2219837	0.183101	0.939619	ENSG00000197746.9

rs3180	Adipose visceral omentum_El	20	0.007092	-4.393	0.119789	2.82386	SPOCK2	Adipose vi	GTEEx_v6	T	C	73762673	10	rs2219837	0.1498	0.948411	ENSG00000107742.8
rs3180	Cells EBV-transformed lympho	20	0.851563	6.333	0.120154	4.075176	NPM1P24	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	-0.21597	0.942041	ENSG00000215086.2
rs3180	Artery aorta_ENSG000001077	20	0.448699	-3.144	0.120986	2.027627	SPOCK2	Artery aor	GTEEx_v6	T	C	73762673	10	rs2219837	0.107215	0.944366	ENSG00000107742.8
rs3180	Artery aorta_ENSG000002137	16	0.340662	2.557	0.122062	1.654048	RPL17P50	Artery aor	GTEEx_v6	A	G	73820622	10	rs3180	-0.08516	0.940444	ENSG00000213700.3
rs7814941	Testis_ENSG00000153310.14	19	0.048095	-1.430	0.122833	0.926761	FAM49B	Testis	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.06349	0.927912	ENSG00000153310.14
rs3180	Brain putamen basal ganglia_	20	0.226233	-4.438	0.12407	2.885544	SPOCK2	Brain puta	GTEEx_v6	T	C	73762673	10	rs2219837	0.151326	0.92054	ENSG00000107742.8
rs3180	Brain cerebellar hemisphere_	1	NA	-13.231	0.124202	8.606055	RP11-152N	Brain cere	GTEEx_v6	C	G	74046191	10	rs1074039	-0.22095	1.055894	ENSG00000227540.1
rs3180	Pancreas_ENSG00000122884.	8	0.591914	7.974	0.124268	5.187959	P4HA1	Pancreas	GTEEx_v6	T	C	73885849	10	rs1668156	-0.14912	1.012536	ENSG00000122884.8
rs3180	Skin not sun exposed suprapu	1	NA	-8.603	0.124974	5.607338	RP11-152N	Skin not su	GTEEx_v6	C	G	74046191	10	rs1074039	-0.14367	1.065166	ENSG00000227540.1
rs7814941	Skin not sun exposed suprapu	20	0.000672	-3.062	0.125361	1.997755	RP11-274N	Skin not su	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.13595	0.920851	ENSG00000224110.3
rs3180	Small intestine terminal ileum	6	0.633786	10.699	0.127677	7.023539	NUDT13	Small intes	GTEEx_v6	G	A	73883196	10	rs1245578	-0.199	0.986017	ENSG00000166321.9
rs3180	Lung_ENSG00000272988.1	20	0.524637	-4.056	0.128011	2.664726	RP11-150C	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	0.138299	0.920244	ENSG00000272988.1
rs3180	Cells EBV-transformed lympho	1	NA	-5.883	0.128332	3.868637	MRPS16	Cells EBV-t	GTEEx_v6	C	G	74046191	10	rs1074039	-0.09825	1.040932	ENSG00000182180.9
rs3180	Pancreas_ENSG00000166295.	20	0.420944	2.461	0.128453	1.618885	ANAPC16	Pancreas	GTEEx_v6	T	C	73762673	10	rs2219837	-0.08392	0.913323	ENSG00000166295.4
rs3180	Heart atrial appendage_ENSG	20	0.806448	-3.635	0.128559	2.391873	UNC5B-AS	Heart atria	GTEEx_v6	T	C	73762673	10	rs2219837	0.12396	0.913765	ENSG00000237512.2
rs3180	Cells transformed fibroblasts_	1	NA	3.039	0.12889	2.001097	DNAJC9	Cells trans	GTEEx_v6	C	G	74046191	10	rs1074039	0.050746	1.047849	ENSG00000213551.4
rs7814941	Vagina_ENSG00000153317.1C	17	0.136154	-2.656	0.129885	1.753793	ASAP1	Vagina	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.11794	0.892715	ENSG00000153317.10
rs3180	Brain cerebellum_ENSG00000	20	0.032514	-6.579	0.130278	4.348473	RP11-150C	Brain cere	GTEEx_v6	T	C	73762673	10	rs2219837	0.224353	0.903017	ENSG00000272988.1
rs3180	Artery coronary_ENSG000001	20	0.502168	-3.761	0.131265	2.491965	SLC29A3	Artery coro	GTEEx_v6	T	C	73762673	10	rs2219837	0.12824	0.901651	ENSG00000198246.7
rs3180	Pituitary_ENSG00000107738.:	20	0.029525	-5.200	0.133381	3.464796	C10orf54	Pituitary	GTEEx_v6	T	C	73762673	10	rs2219837	0.177331	0.88898	ENSG00000107738.15
rs3180	Brain hippocampus_ENSG000	20	0.456264	-4.616	0.133731	3.078476	MCU	Brain hipp	GTEEx_v6	T	C	73762673	10	rs2219837	0.157417	0.88614	ENSG00000156026.10
rs3180	Spleen_ENSG00000237512.2	20	0.292498	7.492	0.134341	5.003801	UNC5B-AS	Spleen	GTEEx_v6	T	C	73762673	10	rs2219837	-0.25547	0.886197	ENSG00000237512.2
rs3180	Adipose subcutaneous_ENSG	20	0.007908	3.778	0.134662	2.525555	C10orf105	Adipose su	GTEEx_v6	T	C	73762673	10	rs2219837	-0.12884	0.896836	ENSG00000214688.4
rs3180	Lung_ENSG00000226701.1	20	0.558341	3.873	0.134823	2.589711	RP11-570C	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	-0.13205	0.895923	ENSG00000226701.1
rs3180	Brain anterior cingulate corte	20	0.269272	4.576	0.134901	3.060792	SPOCK2	Brain ante	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15604	0.879022	ENSG00000107742.8
rs3180	Heart atrial appendage_ENSG	20	0.733168	3.495	0.136391	2.346742	UNC5B	Heart atria	GTEEx_v6	T	C	73762673	10	rs2219837	-0.11919	0.886311	ENSG00000107731.8
rs3180	Cells EBV-transformed lympho	20	0.892255	6.290	0.136895	4.22857	RP11-354E	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	-0.21448	0.881801	ENSG00000272627.1
rs7814941	Brain frontal cortex BA9_ENSC	18	0.587861	4.602	0.13745	3.098224	RP11-473C	Brain front	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.204327	0.870465	ENSG00000254317.1
rs3180	Brain cortex_ENSG000002275	1	NA	-12.704	0.137727	8.559187	RP11-152N	Brain corté	GTEEx_v6	C	G	74046191	10	rs1074039	-0.21217	0.992376	ENSG00000227540.1
rs3180	Muscle skeletal_ENSG000001	8	0.801022	-4.082	0.138247	2.753496	P4HA1	Muscle ske	GTEEx_v6	T	C	73885849	10	rs1668156	0.076327	0.958832	ENSG00000122884.8
rs3180	Skin sun exposed lower leg_El	1	NA	-3.414	0.138552	2.305004	MRPS16	Skin sun ex	GTEEx_v6	C	G	74046191	10	rs1074039	-0.05702	1.001654	ENSG00000182180.9
rs3180	Esophagus mucosa_ENSG0000	1	NA	4.666	0.140323	3.164122	DNAJC9	Esophagus	GTEEx_v6	C	G	74046191	10	rs1074039	0.077919	0.992103	ENSG00000213551.4
rs7814941	Cells EBV-transformed lympho	19	0.391065	-4.377	0.140765	2.971377	LINC00977	Cells EBV-t	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.19433	0.863162	ENSG00000250400.3
rs3180	Testis_ENSG00000272599.1	5	0.250661	8.112	0.140864	5.508682	RP11-152N	Testis	GTEEx_v6	C	T	73899093	10	rs1245515	-0.15088	0.943137	ENSG00000272599.1
rs3180	Uterus_ENSG00000166295.4	20	0.181682	4.658	0.141686	3.169477	ANAPC16	Uterus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15883	0.856542	ENSG00000166295.4
rs3180	Artery tibial_ENSG000001682	20	0.061659	-2.150	0.141987	1.464271	DDIT4	Artery tibi	GTEEx_v6	T	C	73762673	10	rs2219837	0.073321	0.871827	ENSG00000168209.4
rs12310519	Breast mammary tissue_ENSC	11	0.10265	-2.642	0.142636	1.802072	RP11-444C	Breast mai	GTEEx_v6	C	T	23982559	12	rs9804988	0.152967	0.858616	ENSG00000255864.1
rs3180	Brain nucleus accumbens basa	1	NA	16.378	0.143473	11.19482	E1F4A2P2	Brain nuck	GTEEx_v6	C	G	74046191	10	rs1074039	0.273509	0.966243	ENSG00000227382.1
rs3180	Ovary_ENSG00000213700.3	16	0.305162	-5.501	0.143654	3.762154	RPL17P50	Ovary	GTEEx_v6	A	G	73820622	10	rs3180	0.183199	0.855161	ENSG00000213700.3
rs3180	Brain putamen basal ganglia_	20	0.465942	-7.904	0.144157	5.411718	MCU	Brain puta	GTEEx_v6	T	C	73762673	10	rs2219837	0.269517	0.852382	ENSG00000156026.10
rs3180	Prostate_ENSG00000200170.:	20	0.005561	-7.661	0.144964	5.256076	Y_RNA	Prostate	GTEEx_v6	T	C	73762673	10	rs2219837	0.26124	0.851314	ENSG00000200170.1
rs12310519	Pituitary_ENSG00000115934.:	11	0.560072	5.859	0.145557	4.025903	RP11-153K	Pituitary	GTEEx_v6	C	T	23982559	12	rs9804988	-0.33926	0.841306	ENSG00000115934.11
rs3180	Esophagus gastroesophageal j	16	0.151998	3.438	0.146064	2.365482	RPL17P50	Esophagus	GTEEx_v6	A	G	73820622	10	rs3180	-0.1145	0.853484	ENSG00000213700.3
rs3180	Artery coronary_ENSG000001	8	0.201438	5.993	0.146476	4.127145	P4HA1	Artery coro	GTEEx_v6	T	C	73885849	10	rs1668156	-0.11207	0.917541	ENSG00000122884.8
rs3180	Adrenal gland_ENSG00000230	20	0.216431	5.122	0.146897	3.530839	RP11-472C	Adrenal gl	GTEEx_v6	T	C	73762673	10	rs2219837	-0.17465	0.850602	ENSG00000230526.1
rs12310519	Colon transverse_ENSG00000	11	0.482203	-1.742	0.147013	1.201484	SOX5	Colon tran	GTEEx_v6	C	T	23982559	12	rs9804988	0.100882	0.844245	ENSG00000134532.11
rs3180	Brain hypothalamus_ENSG000	20	0.228053	8.154	0.147355	5.62776	DNAJB12	Brain hypc	GTEEx_v6	T	C	73762673	10	rs2219837	-0.27806	0.842181	ENSG00000148719.10
rs3180	Testis_ENSG00000200356.1	1	NA	12.356	0.148817	8.558714	RNU6-833	Testis	GTEEx_v6	C	G	74046191	10	rs1074039	0.206352	0.950856	ENSG00000200356.1
rs3180	Colon sigmoid_ENSG0000010'	20	0.404775	-3.045	0.149651	2.113164	SPOCK2	Colon signr	GTEEx_v6	T	C	73762673	10	rs2219837	0.10382	0.841879	ENSG00000107742.8
rs3180	Brain putamen basal ganglia_	20	0.333526	-3.751	0.15074	2.61017	PSAP	Brain puta	GTEEx_v6	T	C	73762673	10	rs2219837	0.127896	0.832175	ENSG00000197746.9

rs7814941	Brain cortex_ENSG000001476	18	0.27392	5.722	0.150999	3.98474	GSDMC	Brain corte GTeX_v6	A	G	1.31E+08	8	rs1095648	0.254063	0.829055	ENSG00000147697.4
rs7814941	Brain hypothalamus_ENSG00	17	0.142091	4.993	0.151037	3.4772	GSDMC	Brain hypc GTeX_v6	A	G	1.31E+08	8	rs1095648	0.221682	0.825809	ENSG00000147697.4
rs3180	Prostate_ENSG0000213551.4	1	NA	-11.192	0.152259	7.818038	DNAJC9	Prostate GTeX_v6	C	G	74046191	10	rs1074039	-0.18691	0.928656	ENSG00000213551.4
rs7814941	Breast mammary tissue_ENSG	20	0.047989	1.603	0.153505	1.123131	ASAP1	Breast mai GTeX_v6	A	G	1.31E+08	8	rs1095648	0.071173	0.827712	ENSG00000153317.10
rs3180	Muscle skeletal_ENSG000001	6	0.023056	-4.339	0.154568	3.04797	NUDT13	Muscle ske GTeX_v6	G	A	73883196	10	rs1245578	0.080706	0.896689	ENSG00000166321.9
rs3180	Testis_ENSG0000226701.1	20	0.828752	-5.054	0.154927	3.553306	RP11-570C	Testis GTeX_v6	T	C	73762673	10	rs2219837	0.172342	0.827374	ENSG00000226701.1
rs3180	Heart atrial appendage_ENSG	20	0.576217	-1.983	0.155555	1.39659	ASCC1	Heart atria GTeX_v6	T	C	73762673	10	rs2219837	0.067634	0.825568	ENSG00000138303.13
rs3180	Esophagus muscularis_ENSG0	5	0.867802	7.963	0.155658	5.608784	RP11-152N	Esophagus GTeX_v6	C	T	73899093	10	rs1245515	-0.14812	0.890189	ENSG00000272599.1
rs3180	Ovary_ENSG00000166228.4	2	NA	-6.774	0.155849	4.773025	PCBD1	Ovary GTeX_v6	C	T	73646408	10	rs1437267	-0.14835	0.895253	ENSG00000166228.4
rs7814941	Nerve tibial_ENSG00001533	20	0.426306	1.904	0.156194	1.342918	ASAP1	Nerve tibi GTeX_v6	A	G	1.31E+08	8	rs1095648	0.084548	0.821769	ENSG00000153317.10
rs3180	Brain hypothalamus_ENSG00	20	0.022068	-4.665	0.156548	3.292591	CHST3	Brain hypc GTeX_v6	T	C	73762673	10	rs2219837	0.159072	0.81484	ENSG00000122863.5
rs3180	Pancreas_ENSG00000272599.	5	0.885346	-7.719	0.157326	5.458223	RP11-152N	Pancreas GTeX_v6	C	T	73899093	10	rs1245515	0.143566	0.880705	ENSG00000272599.1
rs3180	Breast mammary tissue_ENSG	20	0.021907	-2.332	0.15805	1.651846	ANAPC16	Breast mai GTeX_v6	T	C	73762673	10	rs2219837	0.079516	0.819453	ENSG00000166295.4
rs3180	Ovary_ENSG00000107745.12	20	0.790736	-4.582	0.158321	3.247934	MICU1	Ovary GTeX_v6	T	C	73762673	10	rs2219837	0.156246	0.810909	ENSG00000107745.12
rs3180	Vagina_ENSG00000122884.8	8	0.371711	7.354	0.160005	5.234312	P4HA1	Vagina GTeX_v6	T	C	73858549	10	rs1668156	-0.13753	0.862067	ENSG00000122884.8
rs3180	Brain anterior cingulate cortex_ENSG	20	0.128184	-3.944	0.160461	2.810421	CHST3	Brain ante GTeX_v6	T	C	73762673	10	rs2219837	0.134507	0.801093	ENSG00000122863.5
rs3180	Heart atrial appendage_ENSG	20	0.097314	2.834	0.16148	2.023972	PSAP	Heart atria GTeX_v6	T	C	73762673	10	rs2219837	-0.09663	0.808373	ENSG00000197746.9
rs3180	Adrenal gland_ENSG00000166	20	0.847052	-4.055	0.161803	2.898674	ANAPC16	Adrenal gl GTeX_v6	T	C	73762673	10	rs2219837	0.138287	0.806224	ENSG00000166295.4
rs3180	Brain frontal cortex_BA9_ENSG	6	0.905947	-11.586	0.161999	8.285465	NUDT13	Brain front GTeX_v6	G	A	73883196	10	rs1245578	0.215504	0.859303	ENSG00000166321.9
rs3180	Colon transverse_ENSG00000	20	0.609651	-3.203	0.163534	2.299172	CDH23	Colon tran GTeX_v6	T	C	73762673	10	rs2219837	0.109236	0.8031	ENSG00000107736.15
rs3180	Brain hippocampus_ENSG000	20	0.379304	-3.896	0.163534	2.796409	ASCC1	Brain hipp GTeX_v6	T	C	73762673	10	rs2219837	0.13286	0.795153	ENSG00000138303.13
rs3180	Adrenal gland_ENSG0000010:	20	0.308114	3.861	0.163923	2.773459	C10orf54	Adrenal gl GTeX_v6	T	C	73762673	10	rs2219837	-0.13165	0.800264	ENSG00000107738.15
rs3180	Brain cerebellar hemisphere_	20	0.716737	5.204	0.164808	3.746626	DDIT4	Brain cereb GTeX_v6	T	C	73762673	10	rs2219837	-0.17747	0.793333	ENSG00000168209.4
rs3180	Esophagus muscularis_ENSG0	1	NA	3.848	0.165236	2.772866	MRPS16	Esophagus GTeX_v6	C	G	74046191	10	rs1074039	0.064259	0.889882	ENSG00000182180.9
rs12310519	Adipose subcutaneous_ENSG	11	0.335159	-1.655	0.16565	1.193667	SOX5	Adipose su GTeX_v6	C	T	23982559	12	rs9804988	0.095813	0.793511	ENSG00000134532.11
rs3180	Heart left ventricle_ENSG000	20	0.091539	4.202	0.166132	3.034162	RP11-354E	Heart left GTeX_v6	T	C	73762673	10	rs2219837	-0.14327	0.796725	ENSG000000272627.1
rs3180	Adipose subcutaneous_ENSG	20	0.209087	1.521	0.166451	1.099193	DNAJB12	Adipose su GTeX_v6	T	C	73762673	10	rs2219837	-0.05186	0.798062	ENSG00000148719.10
rs3180	Brain hypothalamus_ENSG00	1	NA	7.795	0.166737	5.637454	DNAJC9	Brain hypc GTeX_v6	C	G	74046191	10	rs1074039	0.130181	0.872607	ENSG00000213551.4
rs3180	Lung_ENSG00000213551.4	1	NA	4.668	0.167016	3.377853	DNAJC9	Lung GTeX_v6	C	G	74046191	10	rs1074039	0.077951	0.884756	ENSG00000213551.4
rs3180	Pituitary_ENSG00000107731.8	20	0.043265	4.304	0.168142	3.122609	UNC5B	Pituitary GTeX_v6	T	C	73762673	10	rs2219837	-0.14675	0.783905	ENSG00000107731.8
rs3180	Ovary_ENSG00000122882.6	1	NA	11.975	0.168613	8.698344	ECD	Ovary GTeX_v6	C	G	74046191	10	rs1074039	0.199979	0.867385	ENSG00000122882.6
rs3180	Brain hippocampus_ENSG000	16	0.444919	-4.440	0.168855	3.226647	RPL17P50	Brain hipp GTeX_v6	A	G	73820622	10	rs3180	0.147836	0.780869	ENSG00000213700.3
rs3180	Whole blood_ENSG00000166	2	NA	-3.074	0.170016	2.240371	PCBD1	Whole blo GTeX_v6	C	T	73646408	10	rs1437267	-0.06732	0.858118	ENSG00000166228.4
rs3180	Adrenal gland_ENSG00000166	2	NA	-8.033	0.170058	5.854962	PCBD1	Adrenal gl GTeX_v6	C	T	73646408	10	rs1437267	-0.17593	0.851879	ENSG00000166228.4
rs3180	Vagina_ENSG00000166321.9	6	0.200618	11.187	0.170239	8.157329	NUDT13	Vagina GTeX_v6	G	A	73883196	10	rs1245578	-0.20808	0.829867	ENSG00000166321.9
rs3180	Nerve tibial_ENSG000002137	16	0.05779	2.037	0.170283	1.485094	RPL17P50	Nerve tibi GTeX_v6	A	G	73820622	10	rs3180	-0.06782	0.787035	ENSG00000213700.3
rs3180	Nerve tibial_ENSG000001982	20	0.041195	2.622	0.170357	1.912271	SLC29A3	Nerve tibi GTeX_v6	T	C	73762673	10	rs2219837	-0.0894	0.786692	ENSG00000198246.7
rs3180	Brain hippocampus_ENSG000	20	0.226508	-4.103	0.171415	3.00033	MICU1	Brain hippoc GTeX_v6	T	C	73762673	10	rs2219837	0.139928	0.773962	ENSG00000107745.12
rs3180	Pancreas_ENSG00000168209.	20	0.364136	2.635	0.172548	1.931792	DDIT4	Pancreas GTeX_v6	T	C	73762673	10	rs2219837	-0.08986	0.777367	ENSG00000168209.4
rs3180	Liver_ENSG00000122863.5	20	0.642606	-3.086	0.174003	2.269713	CHST3	Liver GTeX_v6	T	C	73762673	10	rs2219837	0.105218	0.770047	ENSG00000122863.5
rs12310519	Brain frontal cortex_BA9_ENSG	11	0.389848	2.708	0.174474	1.993912	SOX5	Brain front GTeX_v6	C	T	23982559	12	rs9804988	0.15677	0.761936	ENSG00000134532.11
rs3180	Brain hypothalamus_ENSG00	20	0.23819	-5.529	0.1754	4.080326	CDH23	Brain hypc GTeX_v6	T	C	73762673	10	rs2219837	0.188541	0.763621	ENSG00000107736.15
rs3180	Brain nucleus accumbens basi	20	0.340186	-3.032	0.176167	2.241802	SPOCK2	Brain nuck GTeX_v6	T	C	73762673	10	rs2219837	0.103404	0.763866	ENSG00000107742.8
rs3180	Adipose subcutaneous_ENSG	8	0.313468	-3.743	0.176727	2.770395	P4HA1	Adipose su GTeX_v6	T	C	73858549	10	rs1668156	0.069985	0.820977	ENSG00000122884.8
rs3180	Brain hypothalamus_ENSG00	8	0.175022	11.929	0.178	8.856275	RP11-344N	Brain hypc GTeX_v6	T	C	73865131	10	rs1100017	-0.22188	0.806494	ENSG00000272630.1
rs3180	Adipose subcutaneous_ENSG	1	NA	7.385	0.178012	5.482846	EIF4A2P2	Adipose su GTeX_v6	C	G	74046191	10	rs1074039	0.123327	0.846856	ENSG00000227382.1
rs7814941	Brain frontal cortex_BA9_ENSG	18	0.19338	-1.637	0.178018	1.215052	FAM49B	Brain front GTeX_v6	A	G	1.31E+08	8	rs1095648	-0.07266	0.754486	ENSG00000153310.14
rs3180	Brain cerebellar hemisphere_	20	0.121917	-6.899	0.178955	5.133264	SLC29A3	Brain cereb GTeX_v6	T	C	73762673	10	rs2219837	0.235256	0.756136	ENSG00000198246.7
rs3180	Heart left ventricle_ENSG000	20	0.478896	-2.938	0.179286	2.187998	DDIT4	Heart left GTeX_v6	T	C	73762673	10	rs2219837	0.100199	0.761693	ENSG00000168209.4
rs3180	Testis_ENSG00000122882.6	1	NA	7.286	0.179687	5.422997	ECD	Testis GTeX_v6	C	G	74046191	10	rs1074039	0.121668	0.8372	ENSG00000122882.6

rs7814941	Nerve tibial_ENSG000001533:	20	0.392377	1.195	0.179721	0.890643	FAM49B	Nerve tibi ^g GTEx_v6	A	G	1.31E+08	8	rs1095648	0.053054	0.757856	ENSG00000153310.14	
rs3180	Testis_ENSG00000138315.8	20	0.143167	-3.661	0.179774	2.729416	OIT3	Testis	GTEx_v6	T	C	73762673	10	rs2219837	0.124853	0.759124	ENSG00000138315.8
rs3180	Heart left ventricle_ENSG000	20	0.439002	-4.450	0.179988	3.318628	C10orf105	Heart left\	GTEx_v6	T	C	73762673	10	rs2219837	0.151731	0.759898	ENSG00000214688.4
rs3180	Prostate_ENSG00000148719.:	20	0.472867	-4.441	0.181036	3.320084	DNAJB12	Prostate	GTEx_v6	T	C	73762673	10	rs2219837	0.151433	0.750753	ENSG00000148719.10
rs3180	Cells EBV-transformed lympho	20	0.491436	5.467	0.181879	4.095057	CDH23	Cells EBV-t	GTEx_v6	T	C	73762673	10	rs2219837	-0.18642	0.751848	ENSG00000107736.15
rs7814941	Esophagus muscularis_ENSG0	20	0.427093	-2.224	0.182433	1.668294	ASAP1	Esophagus	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.09876	0.75042	ENSG00000153317.10
rs3180	Skin sun exposed lower leg_EI	20	0.322659	2.493	0.183536	1.874489	UNC5B-AS	Skin sun e\	GTEx_v6	T	C	73762673	10	rs2219837	-0.08501	0.75296	ENSG00000237512.2
rs7814941	Spleen_ENSG00000229140.4	17	0.100688	5.018	0.184146	3.778455	CCDC26	Spleen	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.222806	0.739325	ENSG00000229140.4
rs3180	Esophagus mucosa_ENSG000	20	0.133744	2.336	0.184158	1.759202	DNAJB12	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	-0.07967	0.750613	ENSG00000148719.10
rs3180	Artery tibial_ENSG000001077	20	0.242829	2.422	0.185523	1.829076	MICU1	Artery tibi	GTEx_v6	T	C	73762673	10	rs2219837	-0.08258	0.7478	ENSG00000107745.12
rs12310519	Artery aorta_ENSG000002558	11	0.332736	-2.042	0.185719	1.543107	RP11-444L	Artery aor	GTEx_v6	C	T	23982559	12	rs9804988	0.118236	0.740062	ENSG00000255864.1
rs3180	Vagina_ENSG00000156026.1C	20	0.307949	5.523	0.186422	4.179984	MICU	Vagina	GTEx_v6	T	C	73762673	10	rs2219837	-0.18833	0.736049	ENSG00000156026.10
rs3180	Lung_ENSG00000122863.5	20	0.23006	-2.146	0.186682	1.625557	CHST3	Lung	GTEx_v6	T	C	73762673	10	rs2219837	0.073195	0.744843	ENSG00000122863.5
rs7814941	Colon transverse_ENSG00000	19	0.609165	-1.317	0.186842	0.997592	ASAP1	Colon tran	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.05847	0.738124	ENSG00000153317.10
rs3180	Stomach_ENSG00000166228.	2	NA	6.079	0.187003	4.606848	PCBD1	Stomach	GTEx_v6	C	T	73646408	10	rs1437267	0.133124	0.800522	ENSG00000166228.4
rs3180	Colon transverse_ENSG00000	8	0.468447	-4.351	0.187034	3.297378	P4HA1	Colon tran	GTEx_v6	T	C	73858549	10	rs1668156	0.081356	0.78733	ENSG00000122884.8
rs3180	Brain hypothalamus_ENSG000	20	0.659222	3.658	0.187218	2.773379	ANAPC16	Brain hypc	GTEx_v6	T	C	73762673	10	rs2219837	-0.12473	0.73435	ENSG00000166295.4
rs3180	Heart atrial appendage_ENSG	1	NA	-8.510	0.188559	6.472202	DNAJC9-A ¹	Heart atria	GTEx_v6	C	G	74046191	10	rs1074039	-0.14212	0.809184	ENSG00000236756.4
rs3180	Esophagus gastroesophageal	8	0.259246	8.230	0.188821	6.262598	RP11-344N	Esophagus	GTEx_v6	T	C	73865131	10	rs1100017	-0.15307	0.781454	ENSG00000272630.1
rs3180	Brain hippocampus_ENSG000	8	0.360291	9.948	0.189142	7.575646	RP11-344N	Brain hipp	GTEx_v6	T	C	73865131	10	rs1100017	-0.18503	0.774598	ENSG00000272630.1
rs3180	Adipose subcutaneous_ENSG0	20	0.670317	-1.997	0.190258	1.524976	CHST3	Adipose su	GTEx_v6	T	C	73762673	10	rs2219837	0.068113	0.736357	ENSG00000122863.5
rs3180	Pancreas_ENSG00000107745.	20	0.285469	-3.095	0.190694	2.364924	MICU1	Pancreas	GTEx_v6	T	C	73762673	10	rs2219837	0.105525	0.731731	ENSG00000107745.12
rs3180	Muscle skeletal_ENSG000001:	20	0.769004	-3.001	0.191305	2.296639	OIT3	Muscle ske	GTEx_v6	T	C	73762673	10	rs2219837	0.102337	0.734385	ENSG00000138315.8
rs3180	Brain anterior cingulate cor:	2	NA	7.884	0.192105	6.044319	PCBD1	Brain ante	GTEx_v6	C	T	73646408	10	rs1437267	0.172661	0.775532	ENSG00000166228.4
rs3180	Testis_ENSG00000107736.15	20	0.403643	3.178	0.192142	2.436395	CDH23	Testis	GTEx_v6	T	C	73762673	10	rs2219837	-0.10836	0.728753	ENSG00000107736.15
rs3180	Pituitary_ENSG00000138286.:	1	NA	8.820	0.192858	6.773671	FAM149B1	Pituitary	GTEx_v6	C	G	74046191	10	rs1074039	0.147302	0.790171	ENSG00000138286.10
rs3180	Heart atrial appendage_ENSG	20	0.290932	-2.593	0.193071	1.992438	C10orf54	Heart atria	GTEx_v6	T	C	73762673	10	rs2219837	0.08843	0.726601	ENSG00000107738.15
rs3180	Skin not sun exposed suprapu	1	NA	4.492	0.193391	3.453871	ECD	Skin not su	GTEx_v6	C	G	74046191	10	rs1074039	0.075019	0.796198	ENSG00000122882.6
rs3180	Artery tibial_ENSG000001382	1	NA	3.680	0.193794	2.831822	FAM149B1	Artery tibi	GTEx_v6	C	G	74046191	10	rs1074039	0.061452	0.796828	ENSG00000138286.10
rs3180	Artery coronary_ENSG0000002	16	0.066412	-4.046	0.195757	3.127475	RPL17P50	Artery cor	GTEx_v6	A	G	73820622	10	rs3180	0.134736	0.718903	ENSG00000213700.3
rs7814941	Pancreas_ENSG00000153317.	20	0.069972	-2.914	0.196066	2.254131	ASAP1	Pancreas	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.12939	0.715502	ENSG00000153317.10
rs3180	Cells EBV-transformed lympho	6	0.09746	8.841	0.196968	6.851945	NUDT13	Cells EBV-t	GTEx_v6	G	A	73883196	10	rs1245578	-0.16444	0.758088	ENSG00000166321.9
rs3180	Uterus_ENSG00000122882.6	1	NA	10.666	0.198138	8.288283	ECD	Uterus	GTEx_v6	C	G	74046191	10	rs1074039	0.178122	0.770971	ENSG00000122882.6
rs3180	Artery tibial_ENSG000002726	20	0.630109	-3.411	0.198742	2.654315	RP11-354E	Artery tibi	GTEx_v6	T	C	73762673	10	rs2219837	0.116321	0.716174	ENSG00000272627.1
rs12310519	Pancreas_ENSG00000134532.	11	0.074355	-2.804	0.199363	2.184573	SOX5	Pancreas	GTEx_v6	C	T	23982559	12	rs9804988	0.162329	0.706467	ENSG00000134532.11
rs7814941	Artery coronary_ENSG000001	19	0.330846	4.645	0.199706	3.622354	GSDMC	Artery cor	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.20625	0.706269	ENSG00000147697.4
rs3180	Pancreas_ENSG00000215086.	20	0.517441	4.506	0.200029	3.516198	NPM1P24	Pancreas	GTEx_v6	T	C	73762673	10	rs2219837	-0.15365	0.709988	ENSG00000215086.2
rs3180	Brain putamen basal ganglia_	20	0.102283	-3.842	0.200997	3.004707	CHST3	Brain puta	GTEx_v6	T	C	73762673	10	rs2219837	0.131018	0.702725	ENSG00000122863.5
rs12310519	Thyroid_ENSG00000255864.1	11	0.657158	-2.266	0.201249	1.773211	RP11-444L	Thyroid	GTEx_v6	C	T	23982559	12	rs9804988	0.131211	0.705329	ENSG00000255864.1
rs7814941	Colon sigmoid_ENSG0000015:	17	0.631074	2.983	0.201727	2.336938	FAM49B	Colon sign	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.132465	0.702163	ENSG00000153310.14
rs3180	Spleen_ENSG00000198246.7	20	0.446395	-3.339	0.202839	2.622087	SLC29A3	Spleen	GTEx_v6	T	C	73762673	10	rs2219837	0.113868	0.699765	ENSG00000198246.7
rs3180	Esophagus gastroesophageal	20	0.873404	4.492	0.205518	3.548357	C10orf105	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	-0.15318	0.697316	ENSG00000214688.4
rs3180	Adrenal gland_ENSG0000021:	16	0.073666	-2.970	0.206542	2.351241	RPL17P50	Adrenal gl	GTEx_v6	A	G	73820622	10	rs3180	0.098899	0.695111	ENSG00000213700.3
rs3180	Thyroid_ENSG00000272630.1	8	0.379238	4.847	0.206944	3.840577	RP11-344N	Thyroid	GTEx_v6	T	C	73865131	10	rs1100017	-0.09015	0.736996	ENSG00000272630.1
rs3180	Vagina_ENSG00000168209.4	20	0.293882	-4.164	0.207441	3.303092	DDIT4	Vagina	GTEx_v6	T	C	73762673	10	rs2219837	0.141992	0.688248	ENSG00000168209.4
rs3180	Ovary_ENSG00000197746.9	20	0.685084	-4.066	0.208906	3.235498	PSAP	Ovary	GTEx_v6	T	C	73762673	10	rs2219837	0.138639	0.686107	ENSG00000197746.9
rs3180	Cells EBV-transformed lympho	5	0.048241	7.316	0.209062	5.823957	RP11-152L	Cells EBV-t	GTEx_v6	C	T	73899093	10	rs1245515	-0.13607	0.726966	ENSG00000272599.1
rs3180	Artery tibial_ENSG000002146	20	0.265018	-2.962	0.209556	2.360673	C10orf105	Artery tibi	GTEx_v6	T	C	73762673	10	rs2219837	0.101009	0.691905	ENSG00000214688.4
rs3180	Heart left ventricle_ENSG000	20	0.665998	2.383	0.209973	1.90088	UNC5B-AS	Heart left\	GTEx_v6	T	C	73762673	10	rs2219837	-0.08126	0.68947	ENSG00000237512.2
rs3180	Cells transformed fibroblasts	20	0.602992	-1.502	0.211074	1.200673	DDIT4	Cells trans	GTEx_v6	T	C	73762673	10	rs2219837	0.051204	0.688456	ENSG00000168209.4

rs3180	Lung_ENSG00000166295.4	20	0.968759	1.190	0.211191	0.952102 ANAPC16	Lung	GTEx_v6	T	C	73762673	10	rs2219837	-0.04059	0.688274	ENSG00000166295.4
rs12310519	Brain hippocampus_ENSG000	11	0.756854	-5.187	0.211684	4.152865 RP11-444C	Brain hipp	GTEx_v6	C	T	23982559	12	rs9804988	0.300311	0.674891	ENSG00000255864.1
rs3180	Colon transverse_ENSG00000	1	NA	-9.053	0.211811	7.2508 EIF4A2P2	Colon tran	GTEx_v6	C	G	74046191	10	rs1074039	-0.15119	0.743417	ENSG00000227382.1
rs3180	Stomach_ENSG00000166321.	6	0.488348	5.197	0.212452	4.168351 NUDT13	Stomach	GTEx_v6	G	A	73883196	10	rs1245578	-0.09667	0.720922	ENSG00000166321.9
rs3180	Lung_ENSG00000272627.1	20	0.104414	-2.918	0.212796	2.341738 RP11-354E	Lung	GTEx_v6	T	C	73762673	10	rs2219837	0.09949	0.684811	ENSG00000272627.1
rs3180	Spleen_ENSG00000138286.10	1	NA	-10.242	0.214285	8.247462 FAM149B1	Spleen	GTEx_v6	C	G	74046191	10	rs1074039	-0.17105	0.731682	ENSG00000138286.10
rs3180	Brain nucleus accumbens basa	20	0.747412	4.769	0.214432	3.841742 CDH23	Brain nucle	GTEx_v6	T	C	73762673	10	rs2219837	-0.16264	0.675339	ENSG00000107736.15
rs3180	Testis_ENSG00000156026.10	20	0.926713	-3.353	0.215095	2.704517 MCU	Testis	GTEx_v6	T	C	73762673	10	rs2219837	0.114328	0.67746	ENSG00000156026.10
rs3180	Artery aorta_ENSG000002375	20	0.654778	2.255	0.217135	1.826963 UNC5B-AS	Artery aor	GTEx_v6	T	C	73762673	10	rs2219837	-0.07689	0.674384	ENSG00000237512.2
rs3180	Nerve tibial_ENSG000001077	20	0.967878	2.330	0.212771	1.888191 UNC5B	Nerve tibi	GTEx_v6	T	C	73762673	10	rs2219837	-0.07944	0.675045	ENSG00000107731.8
rs7814941	Brain hypothalamus_ENSG000	17	0.245458	2.275	0.217497	1.845071 FAM49B	Brain hypc	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.101026	0.664317	ENSG00000153310.14
rs3180	Spleen_ENSG00000107745.12	20	0.814602	-4.389	0.217636	3.559794 MICU1	Spleen	GTEx_v6	T	C	73762673	10	rs2219837	0.1149653	0.668192	ENSG00000107745.12
rs3180	Cells EBV-transformed lympho	20	0.303654	5.506	0.217637	4.466421 UNC5B-AS	Cells EBV-t	GTEx_v6	T	C	73762673	10	rs2219837	-0.18777	0.670582	ENSG00000237512.2
rs3180	Nerve tibial_ENSG000001077	20	0.906296	-2.234	0.218442	1.814853 C10orf54	Nerve tibi	GTEx_v6	T	C	73762673	10	rs2219837	0.076163	0.672594	ENSG00000107738.15
rs3180	Heart atrial appendage_ENSG	1	NA	-10.587	0.220844	8.647585 EIF4A2P2	Heart atria	GTEx_v6	C	G	74046191	10	rs1074039	-0.17681	0.719688	ENSG00000227382.1
rs7814941	Prostate_ENSG00000153317.	18	0.553897	-2.542	0.222057	2.081883 ASAP1	Prostate	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.11287	0.656186	ENSG00000153317.10
rs3180	Breast mammary tissue_ENSG	16	0.861316	-2.567	0.223679	2.109573 RPL17P50	Breast mai	GTEx_v6	A	G	73820622	10	rs3180	0.085479	0.660634	ENSG00000213700.3
rs3180	Breast mammary tissue_ENSG	6	0.397398	-5.895	0.224046	4.848276 NUDT13	Breast mai	GTEx_v6	G	A	73883196	10	rs1245578	0.109642	0.693789	ENSG00000166321.9
rs3180	Esophagus gastroesophageal j	20	0.392293	-3.538	0.224644	2.913563 SPOCK2	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	0.120641	0.657064	ENSG00000107742.8
rs3180	Adipose subcutaneous_ENSG	1	NA	-5.143	0.225593	4.243815 RP11-152	Adipose su	GTEx_v6	C	G	74046191	10	rs1074039	-0.08588	0.710779	ENSG00000227540.1
rs3180	Artery coronary_ENSG000002	20	0.392889	4.450	0.225977	3.675589 RP11-354E	Artery cor	GTEx_v6	T	C	73762673	10	rs2219837	-0.15176	0.653892	ENSG00000272627.1
rs3180	Spleen_ENSG00000200170.1	20	0.797875	5.749	0.226479	4.753067 Y_RNA	Spleen	GTEx_v6	T	C	73762673	10	rs2219837	-0.19603	0.650375	ENSG00000200170.1
rs7814941	Colon sigmoid_ENSG0000014	17	0.442862	3.413	0.226602	2.822935 GSDMC	Colon sign	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.151554	0.650186	ENSG00000147697.4
rs3180	Heart left ventricle_ENSG000	8	0.340335	5.724	0.227042	4.738322 P4HA1	Heart left	GTEx_v6	T	C	73858549	10	rs1668156	-0.10704	0.686593	ENSG00000122884.8
rs12310519	Prostate_ENSG00000256321.	11	0.08237	3.668	0.227136	3.036832 RP11-153K	Prostate	GTEx_v6	C	T	23982559	12	rs9804988	-0.21237	0.644961	ENSG00000256321.1
rs3180	Vagina_ENSG00000227540.1	1	NA	13.076	0.228113	10.84949 RP11-152	Vagina	GTEx_v6	C	G	74046191	10	rs1074039	0.218372	0.695988	ENSG00000227540.1
rs3180	Adipose subcutaneous_ENSG	20	0.078494	1.856	0.228781	1.542452 MICU1	Adipose su	GTEx_v6	T	C	73762673	10	rs2219837	-0.0633	0.651962	ENSG00000107745.12
rs7814941	Brain hypothalamus_ENSG000	17	0.974777	2.567	0.229045	2.134151 ASAP1	Brain hypc	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.113975	0.641517	ENSG00000153317.10
rs3180	Breast mammary tissue_ENSG	1	NA	-4.394	0.229591	3.657448 ECD	Breast mai	GTEx_v6	C	G	74046191	10	rs1074039	-0.07338	0.699137	ENSG00000122882.6
rs3180	Uterus_ENSG00000156026.1C	20	0.43301	4.691	0.229654	3.905217 MCU	Uterus	GTEx_v6	T	C	73762673	10	rs2219837	-0.15997	0.641167	ENSG00000156026.10
rs3180	Cells transformed fibroblasts_	8	0.065215	-4.218	0.230199	3.515717 RP11-344N	Cells trans	GTEx_v6	T	C	73865131	10	rs1100017	0.078461	0.681359	ENSG00000272630.1
rs3180	Testis_ENSG00000272988.1	20	0.897081	-4.188	0.230897	3.495293 RP11-150C	Testis	GTEx_v6	T	C	73762673	10	rs2219837	0.142795	0.645365	ENSG00000272988.1
rs3180	Skin sun exposed lower leg_EI	2	NA	-2.663	0.231208	2.223974 PCBD1	Skin sun e)	GTEx_v6	C	T	73646408	10	rs1437267	-0.05831	0.687742	ENSG00000166228.4
rs3180	Ovary_ENSG00000182180.9	1	NA	7.542	0.23123	6.300051 MRPS16	Ovary	GTEx_v6	C	G	74046191	10	rs1074039	0.125958	0.689683	ENSG00000182180.9
rs3180	Ovary_ENSG00000138286.10	1	NA	-6.534	0.233535	5.484912 FAM149B1	Ovary	GTEx_v6	C	G	74046191	10	rs1074039	-0.10912	0.684326	ENSG00000138286.10
rs3180	Small intestine terminal ileum	20	0.316132	4.601	0.23509	3.874671 UNC5B	Small intest	GTEx_v6	T	C	73762673	10	rs2219837	-0.15688	0.631981	ENSG00000107731.8
rs3180	Brain nucleus accumbens basa	20	0.610657	-3.034	0.23528	2.556545 PSAP	Brain nucle	GTEx_v6	T	C	73762673	10	rs2219837	0.103469	0.633784	ENSG00000197746.9
rs3180	Cells transformed fibroblasts_	20	0.286059	-2.014	0.236003	1.699251 SPOCK2	Cells trans	GTEx_v6	T	C	73762673	10	rs2219837	0.068666	0.63758	ENSG00000107742.8
rs3180	Brain nucleus accumbens basa	5	0.829761	11.006	0.236404	9.295812 RP11-152	Brain nucle	GTEx_v6	C	T	73899093	10	rs1245515	-0.20472	0.66199	ENSG00000272599.1
rs3180	Brain cerebellum_ENSG00000	20	0.094208	-4.404	0.236856	3.7233 CDH23	Brain cere	GTEx_v6	T	C	73762673	10	rs2219837	0.150184	0.631704	ENSG00000107736.15
rs7814941	Brain cortex_ENSG000002543	18	0.191214	-4.641	0.237542	3.9289 RP11-473C	Brain cort	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.20604	0.627248	ENSG00000254317.1
rs7814941	Whole blood_ENSG00000243	20	0.216964	-2.125	0.237833	1.800282 RP11-473C	Whole blo	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.09435	0.63199	ENSG00000243402.1
rs3180	Brain cerebellar hemisphere_	1	NA	-14.033	0.240569	11.95772 EIF4A2P2	Brain cere	GTEx_v6	C	G	74046191	10	rs1074039	-0.23435	0.668812	ENSG0000027382.1
rs7814941	Brain caudate basal ganglia_E	18	0.978337	1.030	0.240948	0.878673 FAM49B	Brain caud	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.045748	0.621297	ENSG00000153310.14
rs3180	Vagina_ENSG00000213551.4	1	NA	-8.941	0.241639	7.636428 DNAJC9	Vagina	GTEx_v6	C	G	74046191	10	rs1074039	-0.14932	0.665082	ENSG00000213551.4
rs7814941	Adipose subcutaneous_ENSG	20	0.672499	1.945	0.242275	1.663405 RP11-473C	Adipose su	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.08636	0.623392	ENSG00000254317.1
rs3180	Muscle skeletal_ENSG000001	20	0.368308	-1.223	0.242433	1.045898 DNAJB12	Muscle ske	GTEx_v6	T	C	73762673	10	rs2219837	0.04169	0.625994	ENSG00000148719.10
rs3180	Whole blood_ENSG00000107	20	0.049946	1.126	0.242493	0.96298 MICU1	Whole blo	GTEx_v6	T	C	73762673	10	rs2219837	-0.03838	0.625758	ENSG00000107745.12
rs3180	Brain caudate basal ganglia_E	1	NA	11.113	0.242711	9.512471 EIF4A2P2	Brain caud	GTEx_v6	C	G	74046191	10	rs1074039	0.185584	0.665289	ENSG00000227382.1
rs3180	Cells transformed fibroblasts_	1	NA	1.830	0.243622	1.569401 MRPS16	Cells trans	GTEx_v6	C	G	74046191	10	rs1074039	0.030559	0.668229	ENSG00000182180.9

rs3180	Ovary_ENSG00000237512.2	20	0.675604	4.834	0.243892	4.148308	UNC5B-AS	Ovary	GTEX_v6	T	C	73762673	10	rs2219837	-0.16484	0.616943	ENSG00000237512.2
rs3180	Testis_ENSG00000138308.5	20	0.383615	-2.872	0.244481	2.467312	PLA2G12B	Testis	GTEX_v6	T	C	73762673	10	rs2219837	0.097922	0.619566	ENSG00000138308.5
rs3180	Whole blood_ENSG00000198.	20	0.372467	1.819	0.244512	1.562808	SLC29A3	Whole blo	GTEX_v6	T	C	73762673	10	rs2219837	-0.06202	0.621989	ENSG00000198246.7
rs3180	Brain nucleus accumbens basa	20	0.157022	5.171	0.244768	4.445525	RP11-150C	Brain nuck	GTEX_v6	T	C	73762673	10	rs2219837	-0.17633	0.616111	ENSG00000272988.1
rs3180	Brain anterior cingulate cortex	20	0.47423	-4.715	0.244872	4.054753	UNC5B	Brain ante	GTEX_v6	T	C	73762673	10	rs2219837	0.16079	0.612982	ENSG00000107731.8
rs3180	Testis_ENSG00000107738.15	20	0.695742	-2.513	0.245781	2.165137	C10orf54	Testis	GTEX_v6	T	C	73762673	10	rs2219837	0.085693	0.617176	ENSG00000107738.15
rs3180	Uterus_ENSG00000213551.4	1	NA	-8.602	0.246325	7.41994	DNAJC9	Uterus	GTEX_v6	C	G	74046191	10	rs1074039	-0.14366	0.653092	ENSG00000213551.4
rs3180	Brain cerebellar hemisphere_	20	0.216179	3.751	0.246519	3.237043	DNAJB12	Brain cereb	GTEX_v6	T	C	73762673	10	rs2219837	-0.12792	0.612514	ENSG00000148719.10
rs3180	Small intestine terminal ileum	16	0.673189	-3.912	0.247476	3.383014	RPL17P50	Small intes	GTEX_v6	A	G	73820622	10	rs3180	0.130285	0.609263	ENSG00000213700.3
rs3180	Esophagus mucosa_ENSG0000	1	NA	2.488	0.247935	2.153527	MRPS16	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.041552	0.658387	ENSG00000182180.9
rs3180	Brain putamen basal ganglia_	1	NA	4.313	0.250284	3.751418	FAM149B1	Brain puta	GTEX_v6	C	G	74046191	10	rs1074039	0.072025	0.646748	ENSG00000138286.10
rs3180	Skin sun exposed lower leg_EI	6	0.524463	-3.501	0.250733	3.048301	NUDT13	Skin sun e	GTEX_v6	G	A	73883196	10	rs1245578	0.065122	0.637859	ENSG00000166321.9
rs3180	Artery tibial_ENSG000002726	8	0.267441	-4.836	0.25103	4.21232	RP11-344N	Artery tibi	GTEX_v6	T	C	73865131	10	rs1100017	0.089953	0.637111	ENSG00000272630.1
rs3180	Lung_ENSG00000213700.3	16	0.978235	1.369	0.251034	1.19234	RPL17P50	Lung	GTEX_v6	A	G	73820622	10	rs3180	-0.04558	0.609689	ENSG00000213700.3
rs3180	Ovary_ENSG00000148719.10	20	0.715783	-4.178	0.251176	3.640922	DNAJB12	Ovary	GTEX_v6	T	C	73762673	10	rs2219837	0.142468	0.603843	ENSG00000148719.10
rs3180	Brain caudate basal ganglia_E	20	0.231304	-5.548	0.251346	4.836655	UNC5B-AS	Brain caud	GTEX_v6	T	C	73762673	10	rs2219837	0.189189	0.604887	ENSG00000237512.2
rs3180	Artery aorta_ENSG000001382	1	NA	3.925	0.252173	3.427934	FAM149B1	Artery aor	GTEX_v6	C	G	74046191	10	rs1074039	0.065552	0.64849	ENSG00000138286.10
rs3180	Pancreas_ENSG00000107731.	20	0.6859	2.844	0.253331	2.489897	UNC5B	Pancreas	GTEX_v6	T	C	73762673	10	rs2219837	-0.09699	0.603232	ENSG00000107731.8
rs3180	Colon sigmoid_ENSG0000010	20	0.712772	3.161	0.253871	2.770277	MICU1	Colon sign	GTEX_v6	T	C	73762673	10	rs2219837	-0.10779	0.601853	ENSG00000107745.12
rs3180	Small intestine terminal ileum	5	0.736402	-9.563	0.254053	8.384486	RP11-152N	Small intes	GTEX_v6	C	T	73899093	10	rs1245515	0.177872	0.623746	ENSG00000272599.1
rs3180	Spleen_ENSG00000122882.6	1	NA	7.798	0.254193	6.839389	ECD	Spleen	GTEX_v6	C	G	74046191	10	rs1074039	0.130234	0.639501	ENSG00000122882.6
rs3180	Small intestine terminal ileum	20	0.591414	2.358	0.254366	2.068585	SPOCK2	Small intes	GTEX_v6	T	C	73762673	10	rs2219837	-0.0804	0.597024	ENSG00000107742.8
rs3180	Cells EBV-transformed lympho	20	0.430712	3.948	0.255422	3.4713	C10orf54	Cells EBV-t	GTEX_v6	T	C	73762673	10	rs2219837	-0.13462	0.598615	ENSG00000107738.15
rs3180	Colon transverse_ENSG00000	20	0.905609	2.224	0.255602	1.956	C10orf54	Colon tran	GTEX_v6	T	C	73762673	10	rs2219837	-0.07583	0.599859	ENSG00000107738.15
rs3180	Prostate_ENSG00000221164.	5	0.066326	11.580	0.255662	10.18725	SNORA11	Prostate	GTEX_v6	C	T	73899093	10	rs1245515	-0.21539	0.622158	ENSG00000221164.1
rs3180	Whole blood_ENSG00000107	20	0.182747	0.691	0.257064	0.609866	SPOCK2	Whole blo	GTEX_v6	T	C	73762673	10	rs2219837	-0.02357	0.59927	ENSG00000107742.8
rs3180	Breast mammary tissue_ENSG	20	0.097849	3.393	0.257761	2.99806	UNC5B-AS	Breast mai	GTEX_v6	T	C	73762673	10	rs2219837	-0.1157	0.596415	ENSG00000237512.2
rs3180	Cells EBV-transformed lympho	16	0.084461	3.032	0.258067	2.680495	RPL17P50	Cells EBV-t	GTEX_v6	A	G	73820622	10	rs3180	-0.10095	0.594067	ENSG00000213700.3
rs3180	Whole blood_ENSG00000138	1	NA	-3.222	0.259265	2.856012	FAM149B1	Whole blo	GTEX_v6	C	G	74046191	10	rs1074039	-0.05381	0.635158	ENSG00000138286.10
rs3180	Brain nucleus accumbens basa	20	0.079048	3.376	0.259477	2.994112	C10orf54	Brain nuck	GTEX_v6	T	C	73762673	10	rs2219837	-0.11513	0.59008	ENSG00000107738.15
rs3180	Nerve tibial_ENSG000001662	20	0.75196	1.468	0.259814	1.303052	ANAPC16	Nerve tibia	GTEX_v6	T	C	73762673	10	rs2219837	-0.05007	0.593848	ENSG00000166295.4
rs3180	Heart left ventricle_ENSG000	1	NA	-6.352	0.260011	5.639567	DNAJC9-A	Heart left	GTEX_v6	C	G	74046191	10	rs1074039	-0.10608	0.631959	ENSG00000236756.4
rs3180	Brain caudate basal ganglia_E	20	0.447267	2.382	0.260079	2.115403	UNC5B	Brain caud	GTEX_v6	T	C	73762673	10	rs2219837	-0.08124	0.589631	ENSG00000107731.8
rs7814941	Prostate_ENSG00000147697.	18	0.666834	-2.414	0.260398	2.145228	GSDMC	Prostate	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.1072	0.585876	ENSG00000147697.4
rs3180	Breast mammary tissue_ENSG	8	0.849076	-3.501	0.260427	3.110944	P4HA1	Breast mai	GTEX_v6	T	C	73858549	10	rs1668156	0.065469	0.616705	ENSG00000122884.8
rs3180	Whole blood_ENSG000002150	20	0.327786	-2.816	0.260919	2.504541	NPM1P24	Whole blo	GTEX_v6	T	C	73762673	10	rs2219837	0.096014	0.592528	ENSG00000215086.2
rs3180	Nerve tibial_ENSG000002275	1	NA	4.940	0.262005	4.40448	RP11-152N	Nerve tibia	GTEX_v6	C	G	74046191	10	rs1074039	0.082504	0.628856	ENSG00000227540.1
rs3180	Artery coronary_ENSG000001	6	0.358063	-7.904	0.262753	7.057457	NUDT13	Artery cori	GTEX_v6	G	A	73883196	10	rs1245578	0.147009	0.610892	ENSG00000166321.9
rs7814941	Small intestine terminal ileum	16	0.465144	-3.002	0.262843	2.680723	ASAP1	Small intes	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.13327	0.580419	ENSG00000153317.10
rs3180	Artery tibial_ENSG000002135	1	NA	-4.449	0.263017	3.975079	DNAJC9	Artery tibi	GTEX_v6	C	G	74046191	10	rs1074039	-0.0743	0.627086	ENSG00000213551.4
rs12310519	Brain cortex_ENSG000001345	11	0.175834	1.898	0.266045	1.706498	SOX5	Brain cort	GTEX_v6	C	T	23982559	12	rs9804988	-0.10989	0.576238	ENSG00000134532.11
rs3180	Stomach_ENSG00000122882.	1	NA	-5.306	0.266732	4.777767	ECD	Stomach	GTEX_v6	C	G	74046191	10	rs1074039	-0.08862	0.6179	ENSG00000122882.6
rs3180	Adrenal gland_ENSG00000198	20	0.971792	-3.406	0.26851	3.077893	SLC29A3	Adrenal gl	GTEX_v6	T	C	73762673	10	rs2219837	0.116134	0.576798	ENSG00000198246.7
rs3180	Heart atrial appendage_ENSG	20	0.084647	2.163	0.269534	1.95882	CHST3	Heart atria	GTEX_v6	T	C	73762673	10	rs2219837	-0.07375	0.575713	ENSG00000122863.5
rs3180	Cells transformed fibroblasts_	5	0.445305	-3.318	0.269675	3.006296	RP11-152N	Cells trans	GTEX_v6	C	T	73899093	10	rs1245515	0.061722	0.600821	ENSG00000272599.1
rs3180	Pancreas_ENSG00000156026.	20	0.319252	2.431	0.27027	2.205239	MCU	Pancreas	GTEX_v6	T	C	73762673	10	rs2219837	-0.0829	0.574171	ENSG00000156026.10
rs3180	Vagina_ENSG00000148719.1C	20	0.344997	-3.606	0.270487	3.272815	DNAJB12	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	0.12298	0.570225	ENSG00000148719.10
rs3180	Skin not sun exposed suprapu	6	0.124161	-4.422	0.27095	4.017244	NUDT13	Skin not su	GTEX_v6	G	A	73883196	10	rs1245578	0.082258	0.597539	ENSG00000166321.9
rs12310519	Brain frontal cortex BA9_ENS	11	0.178675	4.003	0.270999	3.636962	RP11-153K	Brain front	GTEX_v6	C	T	23982559	12	rs9804988	-0.2318	0.567794	ENSG00000256321.1
rs3180	Adipose visceral omentum_EI	1	NA	-4.597	0.271575	4.181094	DNAJC9	Adipose vi	GTEX_v6	C	G	74046191	10	rs1074039	-0.07677	0.608777	ENSG00000213551.4

rs3180	Esophagus muscularis_ENSG0	20	0.459089	-1.468	0.272358	1.337709	ANAPC16	Esophagus	GTEX_v6	T	C	73762673	10	rs2219837	0.05007	0.572188	ENSG00000166295.4
rs3180	Brain nucleus accumbens basi	1	NA	-6.463	0.272798	5.893217	ECD	Brain nucle	GTEX_v6	C	G	74046191	10	rs1074039	-0.10793	0.602879	ENSG00000122882.6
rs3180	Thyroid_ENSG00000236756.4	1	NA	3.298	0.273325	3.010396	DNAJC9-A' Thyroid	GTEX_v6	C	G	74046191	10	rs1074039	0.055072	0.606613	ENSG00000236756.4	
rs3180	Esophagus gastroesophageal j	1	NA	6.194	0.2736	5.657395	FAM149B1	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.103436	0.60353	ENSG00000138286.10
rs3180	Brain hypothalamus_ENSG000	20	0.044377	-4.338	0.274319	3.968119	ASCC1	Brain hypc	GTEX_v6	T	C	73762673	10	rs2219837	0.14792	0.564111	ENSG00000138303.13
rs7814941	Brain cerebellar hemisphere_	18	0.919136	-2.711	0.274572	2.481696	ASAP1	Brain cereb	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.12039	0.562633	ENSG00000153317.10
rs7814941	Brain cerebellar hemisphere_	18	0.868993	3.473	0.274658	3.179029	RP11-473C	Brain cereb	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.154191	0.562498	ENSG00000254317.1
rs3180	Adipose visceral omentum_EI	1	NA	8.037	0.275577	7.371363	EIF4A2P2	Adipose vi	GTEX_v6	C	G	74046191	10	rs1074039	0.134219	0.60108	ENSG00000227382.1
rs3180	Brain hippocampus_ENSG000	20	0.216535	3.629	0.276364	3.334147	DNAJB12	Brain hipp	GTEX_v6	T	C	73762673	10	rs2219837	-0.12376	0.560827	ENSG00000148719.10
rs3180	Muscle skeletal_ENSG000002	16	0.143462	1.502	0.278082	1.38509	RPL17P50	Muscle ske	GTEX_v6	A	G	73820622	10	rs3180	-0.05003	0.563883	ENSG00000213700.3
rs3180	Prostate_ENSG00000214688.4	20	0.12883	5.255	0.278129	4.845507	C10orf105	Prostate	GTEX_v6	T	C	73762673	10	rs2219837	-0.1792	0.55875	ENSG00000214688.4
rs3180	Adipose subcutaneous_ENSG0	8	0.304971	4.733	0.278187	4.364541	RP11-344N	Adipose su	GTEX_v6	T	C	73865131	10	rs1100017	-0.08803	0.585476	ENSG00000272630.1
rs3180	Uterus_ENSG00000122863.5	20	0.033959	5.675	0.280599	5.259197	CHST3	Uterus	GTEX_v6	T	C	73762673	10	rs2219837	-0.1935	0.552696	ENSG00000122863.5
rs3180	Spleen_ENSG00000214688.4	20	0.415968	-4.123	0.281417	3.828068	C10orf105	Spleen	GTEX_v6	T	C	73762673	10	rs2219837	0.140607	0.553623	ENSG00000214688.4
rs3180	Heart left ventricle_ENSG000	20	0.170856	-3.429	0.281717	3.185466	OIT3	Heart left\	GTEX_v6	T	C	73762673	10	rs2219837	0.116931	0.556566	ENSG00000138315.8
rs3180	Prostate_ENSG00000138286..	1	NA	-4.692	0.281863	4.360064	FAM149B1	Prostate	GTEX_v6	C	G	74046191	10	rs1074039	-0.07836	0.585449	ENSG00000138286.10
rs12310519	Testis_ENSG00000197503.4	11	0.151367	2.369	0.282224	2.202997	LINC00477	Testis	GTEX_v6	C	T	23982559	12	rs9804988	-0.13716	0.552405	ENSG00000197503.4
rs3180	Brain caudate basal ganglia_E	20	0.231228	-2.797	0.282911	2.604306	ANAPC16	Brain caud	GTEX_v6	T	C	73762673	10	rs2219837	0.095361	0.552123	ENSG00000166295.4
rs3180	Brain cerebellum_ENSG00000	1	NA	4.684	0.282987	4.362903	DNAJC9	Brain cereb	GTEX_v6	C	G	74046191	10	rs1074039	0.078225	0.584659	ENSG00000213551.4
rs7814941	Cells transformed fibroblasts_	20	0.495031	2.552	0.28387	2.381679	RP11-473C	Cells trans	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.113325	0.552213	ENSG00000254317.1
rs3180	Heart atrial appendage_ENSG	1	NA	-5.081	0.285006	4.752297	DNAJC9	Heart atria	GTEX_v6	C	G	74046191	10	rs1074039	-0.08485	0.582836	ENSG00000213551.4
rs3180	Adrenal gland_ENSG0000021:	1	NA	6.132	0.285518	5.741236	DNAJC9	Adrenal gl	GTEX_v6	C	G	74046191	10	rs1074039	0.102399	0.58127	ENSG00000213551.4
rs3180	Ovary_ENSG00000166321.9	6	0.004679	-8.607	0.285836	8.063898	NUDT13	Ovary	GTEX_v6	G	A	73883196	10	rs1245578	0.160083	0.566954	ENSG00000166321.9
rs3180	Vagina_ENSG00000107742.8	20	0.117284	3.587	0.285993	3.361591	SPOCK2	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	-0.12231	0.545558	ENSG00000107742.8
rs3180	Adipose visceral omentum_EI	20	0.640006	-1.970	0.286603	1.848601	MICU1	Adipose vi	GTEX_v6	T	C	73762673	10	rs2219837	0.067173	0.548759	ENSG00000107745.12
rs3180	Vagina_ENSG00000272627.1	20	0.545076	5.113	0.286753	4.799674	RP11-354E	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	-0.17435	0.544383	ENSG000000272627.1
rs3180	Adipose subcutaneous_ENSG0	20	0.821318	-1.233	0.286893	1.157944	ANAPC16	Adipose su	GTEX_v6	T	C	73762673	10	rs2219837	0.042051	0.54944	ENSG00000166295.4
rs3180	Cells transformed fibroblasts_	1	NA	-2.811	0.287562	2.64316	ECD	Cells trans	GTEX_v6	C	G	74046191	10	rs1074039	-0.04694	0.579904	ENSG00000122882.6
rs3180	Uterus_ENSG00000221164.1	5	0.794864	11.506	0.287905	10.82651	SNORA11	Uterus	GTEX_v6	C	T	73899093	10	rs1245515	-0.21401	0.561437	ENSG00000221164.1
rs3180	Heart left ventricle_ENSG000	20	0.264712	2.066	0.288355	1.945414	CDH23	Heart left\	GTEX_v6	T	C	73762673	10	rs2219837	-0.07043	0.546111	ENSG00000107736.15
rs3180	Brain frontal cortex_BA9_ENS	1	NA	-12.009	0.288834	11.32233	EIF4A2P2	Brain front	GTEX_v6	C	G	74046191	10	rs1074039	-0.20056	0.573259	ENSG00000227382.1
rs3180	Adrenal gland_ENSG0000012:	1	NA	6.970	0.29019	6.589564	ECD	Adrenal gl	GTEX_v6	C	G	74046191	10	rs1074039	0.116396	0.572869	ENSG00000122882.6
rs3180	Skin sun exposed lower leg_EI	20	0.484466	1.423	0.290264	1.345278	MCU	Skin sun e)	GTEX_v6	T	C	73762673	10	rs2219837	-0.04851	0.544204	ENSG00000156026.10
rs3180	Brain hypothalamus_ENSG000	20	0.440258	-2.819	0.290356	2.666351	SPOCK2	Brain hypc	GTEX_v6	T	C	73762673	10	rs2219837	0.096136	0.538976	ENSG00000107742.8
rs3180	Nerve tibial_ENSG000001228	20	0.01233	1.597	0.290604	1.510919	CHST3	Nerve tibi	GTEX_v6	T	C	73762673	10	rs2219837	-0.05445	0.543353	ENSG00000122863.5
rs3180	Whole blood_ENSG000002727	5	0.383536	4.959	0.291794	4.704024	RP11-152N	Whole blo	GTEX_v6	C	T	73899093	10	rs1245515	-0.09224	0.561961	ENSG00000272599.1
rs3180	Liver_ENSG00000166321.9	6	0.913333	6.675	0.292375	6.339431	NUDT13	Liver	GTEX_v6	G	A	73883196	10	rs1245578	-0.12415	0.556865	ENSG00000166321.9
rs3180	Artery coronary_ENSG000002	8	0.690348	-7.013	0.295901	6.70907	RP11-344N	Artery cor	GTEX_v6	T	C	73865131	10	rs1100017	0.130437	0.552194	ENSG00000272630.1
rs3180	Esophagus muscularis_ENSG0	1	NA	4.828	0.297503	4.634745	RP11-152N	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.080636	0.561754	ENSG00000227540.1
rs3180	Brain frontal cortex_BA9_ENS	1	NA	-7.892	0.297724	7.578773	DNAJC9-A'	Brain front	GTEX_v6	C	G	74046191	10	rs1074039	-0.1318	0.557746	ENSG00000236756.4
rs3180	Brain cerebellar hemisphere_	20	0.317667	-3.100	0.297992	2.978511	C10orf54	Brain cereb	GTEX_v6	T	C	73762673	10	rs2219837	0.105706	0.528251	ENSG00000107738.15
rs3180	Brain caudate basal ganglia_E	1	NA	-8.196	0.29979	7.904563	RP11-152N	Brain caud	GTEX_v6	C	G	74046191	10	rs1074039	-0.13688	0.554823	ENSG00000227540.1
rs3180	Adrenal gland_ENSG0000022:	1	NA	6.797	0.300567	6.565603	RP11-152N	Adrenal gl	GTEX_v6	C	G	74046191	10	rs1074039	0.113507	0.554801	ENSG00000227540.1
rs3180	Skin not sun exposed suprapu	1	NA	2.739	0.300878	2.647531	MRPS16	Skin not su	GTEX_v6	C	G	74046191	10	rs1074039	0.045742	0.555623	ENSG00000182180.9
rs3180	Uterus_ENSG00000122884.8	8	0.180329	-6.216	0.301885	6.020706	P4HA1	Uterus	GTEX_v6	T	C	73858549	10	rs1668156	0.116235	0.538267	ENSG00000122884.8
rs3180	Brain frontal cortex_BA9_ENS	20	0.2776	2.266	0.301907	2.195319	SPOCK2	Brain front	GTEX_v6	T	C	73762673	10	rs2219837	-0.07728	0.522702	ENSG00000107742.8
rs3180	Skin not sun exposed suprapu	20	0.302965	1.776	0.301936	1.72012	DNAJB12	Skin not su	GTEX_v6	T	C	73762673	10	rs2219837	-0.06055	0.525572	ENSG00000148719.10
rs3180	Thyroid_ENSG00000138303.1	20	0.000657	-1.494	0.301946	1.447105	ASCC1	Thyroid	GTEX_v6	T	C	73762673	10	rs2219837	0.050939	0.526313	ENSG00000138303.13
rs3180	Brain hippocampus_ENSG000	20	0.736427	-2.816	0.301977	2.72801	PSAP	Brain hippoc	GTEX_v6	T	C	73762673	10	rs2219837	0.096021	0.521636	ENSG00000197746.9
rs3180	Liver_ENSG00000156026.10	20	0.225247	2.672	0.302043	2.589357	MCU	Liver	GTEX_v6	T	C	73762673	10	rs2219837	-0.09113	0.522847	ENSG00000156026.10

rs3180	Stomach_ENSG00000122884.	8	0.673425	3.157	0.303198	3.06631	P4HA1	Stomach	GTEEx_v6	T	C	73858549	10	rs1668156	-0.05904	0.541128	ENSG00000122884.8
rs3180	Artery tibial_ENSG000001977	20	0.198774	-1.441	0.303606	1.400326	PSAP	Artery tibi	GTEEx_v6	T	C	73762673	10	rs2219837	0.049123	0.523895	ENSG00000197746.9
rs3180	Skin sun exposed lower leg_EI	20	0.509555	-1.310	0.303737	1.273787	DDIT4	Skin sun e	GTEEx_v6	T	C	73762673	10	rs2219837	0.044672	0.523798	ENSG00000168209.4
rs3180	Brain hippocampus_ENSG000	1	NA	-6.731	0.303932	6.547506	MRPS16	Brain hipp	GTEEx_v6	C	G	74046191	10	rs1074039	-0.11241	0.546193	ENSG00000182180.9
rs12310519	Lung_ENSG00000255745.1	11	0.238045	-1.651	0.304165	1.606515	RP11-625L	Lung	GTEEx_v6	C	T	23982559	12	rs9804988	0.095579	0.520763	ENSG00000255745.1
rs3180	Colon sigmoid_ENSG0000027	20	0.474115	4.130	0.305109	4.026868	RP11-354E	Colon sign	GTEEx_v6	T	C	73762673	10	rs2219837	-0.14082	0.519627	ENSG00000272627.1
rs7814941	Artery coronary_ENSG000002	19	0.082681	-3.510	0.30545	3.425315	RP11-473C	Artery coro	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.15586	0.517372	ENSG00000254317.1
rs3180	Prostate_ENSG00000138303..	20	0.035293	2.775	0.305699	2.709085	ASCC1	Prostate	GTEEx_v6	T	C	73762673	10	rs2219837	-0.09462	0.516865	ENSG00000138303.13
rs3180	Brain frontal cortex_BA9_ENS	1	NA	-4.590	0.306847	4.49153	FAM149B1	Brain front	GTEEx_v6	C	G	74046191	10	rs1074039	-0.07665	0.542406	ENSG00000138286.10
rs3180	Brain cortex_ENSG000001382	1	NA	-5.886	0.306894	5.760327	FAM149B1	Brain corte	GTEEx_v6	C	G	74046191	10	rs1074039	-0.09829	0.542628	ENSG00000138286.10
rs7814941	Pituitary_ENSG00000153317..	18	0.593584	2.192	0.306995	2.14549	ASAP1	Pituitary	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.097312	0.513401	ENSG00000153317.10
rs3180	Brain frontal cortex_BA9_ENS	1	NA	-5.283	0.30703	5.172204	ECD	Brain front	GTEEx_v6	C	G	74046191	10	rs1074039	-0.08823	0.542103	ENSG00000122882.6
rs3180	Skin sun exposed lower leg_EI	20	0.401478	-1.705	0.307587	1.671558	SPOCK2	Skin sun e	GTEEx_v6	T	C	73762673	10	rs2219837	0.058157	0.518142	ENSG00000107742.8
rs3180	Brain anterior cingulate corte	5	0.10983	10.603	0.308117	10.40377	RP11-152N	Brain ante	GTEEx_v6	C	T	73899093	10	rs1245515	-0.19722	0.528892	ENSG00000272599.1
rs3180	Brain cerebellum_ENSG00000	20	0.091117	-2.330	0.309621	2.293572	ANAPC16	Brain cere	GTEEx_v6	T	C	73762673	10	rs2219837	0.079464	0.5122	ENSG00000166295.4
rs12310519	Vagina_ENSG00000255864.1	11	0.447768	2.386	0.309636	2.348074	RP11-444L	Vagina	GTEEx_v6	C	T	23982559	12	rs9804988	-0.13813	0.508347	ENSG00000255864.1
rs3180	Nerve tibial_ENSG000001663	6	0.122073	-4.084	0.31122	4.032957	NUDT13	Nerve tibi	GTEEx_v6	G	A	73883196	10	rs1245578	0.075963	0.529731	ENSG00000166321.9
rs3180	Esophagus gastroesophageal_j	8	0.433519	-3.777	0.311306	3.730269	P4HA1	Esophagus	GTEEx_v6	T	C	73858549	10	rs1668156	0.070627	0.527521	ENSG00000122884.8
rs3180	Ovary_ENSG00000214688.4	20	0.681555	4.540	0.312697	4.496957	C10orf105	Ovary	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15482	0.506688	ENSG00000214688.4
rs3180	Skin not sun exposed suprapu	1	NA	5.370	0.313151	5.323712	DNAJC9-A	Skin not su	GTEEx_v6	C	G	74046191	10	rs1074039	0.089673	0.535142	ENSG00000236756.4
rs3180	Brain nucleus accumbens basi	20	0.082678	-2.729	0.313561	2.707916	C10orf105	Brain nuk	GTEEx_v6	T	C	73762673	10	rs2219837	0.093058	0.505996	ENSG00000214688.4
rs3180	Artery tibial_ENSG000001077	20	0.128714	-1.168	0.313783	1.159066	UNC5B	Artery tibi	GTEEx_v6	T	C	73762673	10	rs2219837	0.039814	0.509101	ENSG00000107731.8
rs3180	Brain caudate basal ganglia_E	20	0.534481	-3.256	0.313888	3.232888	SLC29A3	Brain caud	GTEEx_v6	T	C	73762673	10	rs2219837	0.111024	0.505964	ENSG00000198246.7
rs3180	Spleen_ENSG00000148719.10	20	0.030021	-3.501	0.313898	3.476743	DNAJB12	Spleen	GTEEx_v6	T	C	73762673	10	rs2219837	0.119396	0.505236	ENSG00000148719.10
rs7814941	Muscle skeletal_ENSG000001!	20	0.107897	0.854	0.314183	0.848094	FAM49B	Muscle ske	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.0379	0.507409	ENSG00000153310.14
rs7814941	Cells EBV-transformed lympho	19	0.196178	-3.608	0.314937	3.590228	RP11-473C	Cells EBV-t	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.16019	0.503715	ENSG00000254317.1
rs3180	Adipose subcutaneous_ENSG0	20	0.06267	-1.576	0.315184	1.569494	DDIT4	Adipose su	GTEEx_v6	T	C	73762673	10	rs2219837	0.053756	0.507173	ENSG00000168209.4
rs3180	Vagina_ENSG00000138286.1C	1	NA	-6.919	0.316393	6.906056	FAM149B1	Vagina	GTEEx_v6	C	G	74046191	10	rs1074039	-0.11555	0.525851	ENSG00000138286.10
rs3180	Thyroid_ENSG00000215086.2	20	0.37657	-2.501	0.31652	2.497195	NPM1P24	Thyroid	GTEEx_v6	T	C	73762673	10	rs2219837	0.085294	0.505161	ENSG00000215086.2
rs3180	Heart left ventricle_ENSG000	5	0.711222	6.637	0.316733	6.629178	SNORA11	Heart left \	GTEEx_v6	C	T	73899093	10	rs1245515	-0.12345	0.520484	ENSG00000221164.1
rs3180	Whole blood_ENSG00000226	20	0.158624	-2.416	0.316765	2.412812	RP11-570C	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	0.08237	0.505106	ENSG00000226701.1
rs3180	Heart left ventricle_ENSG000	6	0.728606	4.017	0.316923	4.014275	NUDT13	Heart left \	GTEEx_v6	G	A	73883196	10	rs1245578	-0.07473	0.520193	ENSG00000166321.9
rs7814941	Cells EBV-transformed lympho	19	0.236697	-2.409	0.317323	2.408578	CCDC26	Cells EBV-t	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.10694	0.500382	ENSG00000229140.4
rs3180	Heart atrial appendage_ENSG	6	0.779804	-4.106	0.318931	4.119876	NUDT13	Heart atria	GTEEx_v6	G	A	73883196	10	rs1245578	0.076374	0.516534	ENSG00000166321.9
rs3180	Brain frontal cortex_BA9_ENS	20	0.001973	2.510	0.319279	2.520537	ASCC1	Brain front	GTEEx_v6	T	C	73762673	10	rs2219837	-0.0856	0.497931	ENSG00000138303.13
rs7814941	Spleen_ENSG00000250400.3	17	0.302884	-3.703	0.319714	3.721525	LINC00977	Spleen	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.16442	0.495743	ENSG00000250400.3
rs3180	Cells EBV-transformed lympho	1	NA	6.503	0.320569	6.546806	FAM149B1	Cells EBV-t	GTEEx_v6	C	G	74046191	10	rs1074039	0.108598	0.521578	ENSG00000138286.10
rs3180	Brain frontal cortex_BA9_ENS	20	0.09109	2.727	0.320747	2.746797	PSAP	Brain front	GTEEx_v6	T	C	73762673	10	rs2219837	-0.093	0.495903	ENSG00000197746.9
rs3180	Muscle skeletal_ENSG000001	20	0.151266	-1.381	0.321248	1.392688	ASCC1	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	0.047106	0.498883	ENSG00000138303.13
rs3180	Testis_ENSG00000221164.1	5	0.096839	-6.407	0.321264	6.459547	SNORA11	Testis	GTEEx_v6	C	T	73899093	10	rs1245515	0.11917	0.512979	ENSG00000221164.1
rs7814941	Liver_ENSG00000153317.10	17	0.131547	1.959	0.321618	1.976371	ASAP1	Liver	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.086973	0.493655	ENSG00000153317.10
rs3180	Brain cerebellar hemisphere_	20	0.284295	4.806	0.322883	4.861764	Y_RNA	Brain cereb	GTEEx_v6	T	C	73762673	10	rs2219837	-0.16389	0.492762	ENSG00000200170.1
rs3180	Brain hippocampus_ENSG000	20	0.018971	3.500	0.323513	3.544855	DDIT4	Brain hippoc	GTEEx_v6	T	C	73762673	10	rs2219837	-0.11934	0.491245	ENSG00000168209.4
rs3180	Breast mammary tissue_ENSG	20	0.334324	1.621	0.324953	1.646803	PSAP	Breast mai	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05528	0.492537	ENSG00000197746.9
rs3180	Nerve tibial_ENSG000002367!	1	NA	-4.013	0.326217	4.087192	DNAJC9-A	Nerve tibi	GTEEx_v6	C	G	74046191	10	rs1074039	-0.06701	0.514967	ENSG00000236756.4
rs12310519	Brain cortex_ENSG000002563	11	0.365371	-3.229	0.327479	3.297976	RP11-153K	Brain cort	GTEEx_v6	C	T	23982559	12	rs9804988	0.186982	0.485082	ENSG00000256321.1
rs3180	Brain hypothalamus_ENSG00	20	0.483832	-2.257	0.328597	2.31046	PSAP	Brain hypc	GTEEx_v6	T	C	73762673	10	rs2219837	0.07697	0.484375	ENSG00000197746.9
rs3180	Vagina_ENSG00000237512.2	20	0.718437	-2.604	0.328621	2.665249	UNC5B-AS	Vagina	GTEEx_v6	T	C	73762673	10	rs2219837	0.088785	0.484252	ENSG000000237512.2
rs3180	Colon sigmoid_ENSG0000022	5	0.973564	-6.962	0.330277	7.150594	SNORA11	Colon sign	GTEEx_v6	C	T	73899093	10	rs1245515	0.129484	0.499104	ENSG00000221164.1
rs3180	Brain hippocampus_ENSG000	8	0.608351	5.243	0.330676	5.389909	P4HA1	Brain hippoc	GTEEx_v6	T	C	73858549	10	rs1668156	-0.09805	0.495929	ENSG00000122884.8

rs3180	Artery tibial_ENSG000002375	20	0.869869	1.654	0.33076	1.700344	UNC5B-AS	Artery tibi; GTEx_v6	T	C	73762673	10	rs2219837	-0.05639	0.485496	ENSG00000237512.2	
rs3180	Nerve tibial_ENSG000002267	20	0.145339	-2.734	0.330782	2.811389	RP11-570C	Nerve tibi; GTEx_v6	T	C	73762673	10	rs2219837	0.093236	0.485293	ENSG00000226701.1	
rs3180	Skin not sun exposed suprapu	20	0.095761	2.002	0.33159	2.062462	CHST3	Skin not su	GTEx_v6	T	C	73762673	10	rs2219837	-0.06828	0.483695	ENSG00000122863.5
rs12310519	Colon sigmoid_ENSG0000013	11	0.35586	2.407	0.33339	2.488735	SOX5	Colon sigm	GTEx_v6	C	T	23982559	12	rs9804988	-0.13939	0.478386	ENSG00000134532.11
rs3180	Uterus_ENSG00000197746.9	20	0.617389	-2.524	0.333482	2.609788	PSAP	Uterus	GTEx_v6	T	C	73762673	10	rs2219837	0.086068	0.476821	ENSG00000197746.9
rs3180	Testis_ENSG00000182180.9	1	NA	4.717	0.33389	4.881541	MRPS16	Testis	GTEx_v6	C	G	74046191	10	rs1074039	0.078775	0.502022	ENSG00000182180.9
rs3180	Brain cerebellar hemisphere_	8	0.307788	7.297	0.336088	7.585942	RP11-344N	Brain cere	GTEx_v6	T	C	73865131	10	rs1100017	-0.13573	0.489078	ENSG00000272630.1
rs3180	Brain anterior cingulate corre	6	0.063482	-8.320	0.336411	8.654894	NUDT13	Brain ante	GTEx_v6	G	A	73883196	10	rs1245578	0.154748	0.48701	ENSG00000166321.9
rs7814941	Thyroid_ENSG00000153310.1	20	0.347014	1.093	0.336903	1.138627	FAM49B	Thyroid	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.048548	0.476003	ENSG00000153310.14
rs3180	Liver_ENSG00000213551.4	1	NA	-4.669	0.337817	4.871106	DNAJC9	Liver	GTEx_v6	C	G	74046191	10	rs1074039	-0.07797	0.494511	ENSG00000213551.4
rs3180	Brain putamen basal ganglia_	20	0.421141	-3.747	0.337897	3.910215	SLC29A3	Brain puta	GTEx_v6	T	C	73762673	10	rs2219837	0.127782	0.47217	ENSG00000198246.7
rs3180	Heart left ventricle_ENSG000	5	0.128831	4.726	0.338097	4.933828	RP11-152N	Heart left	GTEx_v6	C	T	73899093	10	rs1245515	-0.08791	0.488903	ENSG00000272599.1
rs3180	Nerve tibial_ENSG000001077	20	0.678996	2.363	0.338574	2.469105	CDH23	Nerve tibi	GTEx_v6	T	C	73762673	10	rs2219837	-0.08057	0.474888	ENSG00000107736.15
rs3180	Heart atrial appendage_ENSG	20	0.787935	2.056	0.338814	2.14998	DNAJB12	Heart atria	GTEx_v6	T	C	73762673	10	rs2219837	-0.07013	0.47351	ENSG00000148719.10
rs7814941	Brain cerebellum_ENSG00000	18	0.445915	-2.316	0.339508	2.424557	ASAP1	Brain cere	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.10282	0.470167	ENSG00000153317.10
rs3180	Skin sun exposed lower leg_EI	20	0.680359	-2.295	0.339876	2.405092	RP11-354E	Skin sun es	GTEx_v6	T	C	73762673	10	rs2219837	0.078275	0.473423	ENSG00000272627.1
rs12310519	Testis_ENSG00000134532.11	11	0.605814	1.474	0.340312	1.545299	SOX5	Testis	GTEx_v6	C	T	23982559	12	rs9804988	-0.08532	0.469807	ENSG00000134532.11
rs3180	Uterus_ENSG00000236756.4	1	NA	-7.222	0.342895	7.614045	DNAJC9-A'	Uterus	GTEx_v6	C	G	74046191	10	rs1074039	-0.1206	0.484879	ENSG00000236756.4
rs3180	Brain cerebellum_ENSG00000	1	NA	7.346	0.343351	7.752358	DNAJC9-A'	Brain cere	GTEx_v6	C	G	74046191	10	rs1074039	0.122676	0.486764	ENSG00000236756.4
rs3180	Brain putamen basal ganglia_	20	0.058769	5.469	0.344202	5.782194	RP11-150C	Brain puta	GTEx_v6	T	C	73762673	10	rs2219837	-0.18651	0.464033	ENSG00000272988.1
rs3180	Nerve tibial_ENSG0000021508	20	0.62911	2.771	0.344246	2.929386	NPM1P24	Nerve tibi	GTEx_v6	T	C	73762673	10	rs2219837	-0.09448	0.467471	ENSG00000215086.2
rs12310519	Small intestine terminal ileum	11	0.126576	3.332	0.344783	3.52669	RP11-444C	Small intes	GTEx_v6	C	T	23982559	12	rs9804988	-0.19292	0.461205	ENSG00000255864.1
rs3180	Small intestine terminal ileum	1	NA	-4.403	0.345114	4.66333	MRPS16	Small intes	GTEx_v6	C	G	74046191	10	rs1074039	-0.07353	0.482404	ENSG00000182180.9
rs3180	Whole blood_ENSG00000227	1	NA	4.374	0.345548	4.63668	RP11-152N	Whole blo	GTEx_v6	C	G	74046191	10	rs1074039	0.073039	0.486423	ENSG00000227540.1
rs3180	Liver_ENSG00000213700.3	16	0.395413	-3.103	0.346605	3.296908	RPL17P50	Liver	GTEx_v6	A	G	73820622	10	rs3180	0.103331	0.461963	ENSG00000213700.3
rs3180	Cells transformed fibroblasts_	1	NA	-4.708	0.349476	5.03254	EIF4A2P2	Cells trans	GTEx_v6	C	G	74046191	10	rs1074039	-0.07863	0.480474	ENSG00000227382.1
rs3180	Small intestine terminal ileum	20	0.034134	1.281	0.351289	1.374676	OIT3	Small intes	GTEx_v6	T	C	73762673	10	rs2219837	-0.04369	0.454643	ENSG00000138315.8
rs3180	Brain caudate basal ganglia_E	20	0.025196	3.375	0.351527	3.622726	MICU1	Brain caud	GTEx_v6	T	C	73762673	10	rs2219837	-0.11509	0.455841	ENSG00000107745.12
rs7814941	Adipose subcutaneous_ENSG	20	0.853593	0.725	0.352409	0.779684	FAM49B	Adipose su	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.032192	0.456139	ENSG00000153310.14
rs12310519	Prostate_ENSG00000255864.	11	0.181523	-3.403	0.352463	3.659343	RP11-444C	Prostate	GTEx_v6	C	T	23982559	12	rs9804988	0.197007	0.452458	ENSG00000255864.1
rs3180	Brain caudate basal ganglia_E	1	NA	-6.060	0.352645	6.519319	DNAJC9	Brain caud	GTEx_v6	C	G	74046191	10	rs1074039	-0.10119	0.47342	ENSG00000213551.4
rs3180	Brain hypothalamus_ENSG00	20	0.697746	-4.525	0.353064	4.872522	SLC29A3	Brain hypc	GTEx_v6	T	C	73762673	10	rs2219837	0.1543	0.452769	ENSG00000198246.7
rs3180	Pituitary_ENSG00000236756.	1	NA	-5.071	0.354002	5.471141	DNAJC9-A'	Pituitary	GTEx_v6	C	G	74046191	10	rs1074039	-0.08468	0.470765	ENSG00000236756.4
rs7814941	Artery coronary_ENSG000001	19	0.597848	2.704	0.35465	2.921624	ASAP1	Artery cor	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.12007	0.451527	ENSG00000153317.10
rs3180	Heart left ventricle_ENSG000	20	0.321153	1.618	0.354781	1.748009	PSAP	Heart left	GTEx_v6	T	C	73762673	10	rs2219837	-0.05516	0.45351	ENSG00000197746.9
rs3180	Heart left ventricle_ENSG000	20	0.8394	-2.208	0.355096	2.387966	PLA2G12B	Heart left	GTEx_v6	T	C	73762673	10	rs2219837	0.075302	0.453114	ENSG00000138308.5
rs7814941	Pancreas_ENSG00000254317.	20	0.607993	-2.596	0.355858	2.811441	RP11-473C	Pancreas	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.11525	0.450445	ENSG00000254317.1
rs3180	Brain cortex_ENSG000002137	16	0.744465	3.044	0.355983	3.298062	RPL17P50	Brain cort	GTEx_v6	A	G	73820622	10	rs3180	-0.10137	0.450125	ENSG00000213700.3
rs3180	Liver_ENSG00000138315.8	20	0.923056	-2.085	0.356239	2.259485	OIT3	Liver	GTEx_v6	T	C	73762673	10	rs2219837	0.071082	0.449823	ENSG00000138315.8
rs7814941	Adipose subcutaneous_ENSG	20	0.645673	1.654	0.356357	1.793808	GSDMC	Adipose su	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.073459	0.451199	ENSG00000147697.4
rs3180	Esophagus mucosa_ENSG000	20	0.045513	-2.079	0.357348	2.258803	CDH23	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	0.070896	0.450751	ENSG00000107736.15
rs3180	Brain hypothalamus_ENSG00	20	0.029931	6.147	0.35766	6.682294	UNC5B-AS	Brain hypc	GTEx_v6	T	C	73762673	10	rs2219837	-0.2096	0.447086	ENSG00000237512.2
rs3180	Brain hippocampus_ENSG00	1	NA	5.740	0.357866	6.242441	DNAJC9	Brain hipp	GTEx_v6	C	G	74046191	10	rs1074039	0.09585	0.464499	ENSG00000213551.4
rs3180	Pancreas_ENSG00000197746.	20	0.601919	-1.749	0.358609	1.905159	PSAP	Pancreas	GTEx_v6	T	C	73762673	10	rs2219837	0.05964	0.448087	ENSG00000197746.9
rs7814941	Brain anterior cingulate corre	16	0.511041	-3.125	0.359397	3.409335	ASAP1	Brain ante	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.13874	0.443118	ENSG00000153317.10
rs3180	Breast mammary tissue_ENSG	1	NA	-4.447	0.359528	4.853751	DNAJC9-A'	Breast mai	GTEx_v6	C	G	74046191	10	rs1074039	-0.07427	0.465648	ENSG00000236756.4
rs3180	Brain putamen basal ganglia_	1	NA	-7.359	0.359847	8.03671	DNAJC9	Brain puta	GTEx_v6	C	G	74046191	10	rs1074039	-0.12289	0.462374	ENSG00000213551.4
rs3180	Brain caudate basal ganglia_E	20	0.734533	3.956	0.361329	4.333246	CDH23	Brain caud	GTEx_v6	T	C	73762673	10	rs2219837	-0.13488	0.443699	ENSG00000107736.15
rs3180	Lung_ENSG00000237512.2	20	0.705428	1.845	0.361818	2.023287	UNC5B-AS	Lung	GTEx_v6	T	C	73762673	10	rs2219837	-0.06292	0.445393	ENSG00000237512.2
rs3180	Brain frontal cortex BA9_ENSG	20	0.131645	-3.073	0.362249	3.372783	UNC5B	Brain front	GTEx_v6	T	C	73762673	10	rs2219837	0.104786	0.442186	ENSG00000107731.8

rs3180	Artery tibial_ENSG000002725	5	0.814074	-4.266	0.362254	4.682108	RP11-152N	Artery tibi; GTEx_v6	C	T	73899093	10	rs1245515	0.079343	0.456544	ENSG00000272599.1	
rs3180	Artery coronary_ENSG000002	20	0.485334	-3.137	0.363126	3.44896	C10orf105	Artery coro; GTEx_v6	T	C	73762673	10	rs2219837	0.106957	0.442148	ENSG00000214688.4	
rs3180	Adrenal gland_ENSG0000018;	1	NA	-3.367	0.363202	3.703151	MRPS16	Adrenal gl; GTEx_v6	C	G	74046191	10	rs1074039	-0.05623	0.459842	ENSG00000182180.9	
rs3180	Brain cerebellar hemisphere_	20	0.79849	2.242	0.363381	2.466282	PSAP	Brain cereb; GTEx_v6	T	C	73762673	10	rs2219837	-0.07644	0.440646	ENSG00000197746.9	
rs3180	Prostate_ENSG00000166321.!	6	0.79282	6.515	0.363749	7.172819	NUDT13	Prostate	GTEx_v6	G	A	73883196	10	rs1245578	-0.12117	0.451522	ENSG00000166321.9
rs3180	Liver_ENSG00000221164.1	5	0.408833	8.196	0.364147	9.031981	SNORA11	Liver	GTEx_v6	C	T	73899093	10	rs1245515	-0.15245	0.451507	ENSG00000221164.1
rs3180	Lung_ENSG00000168209.4	20	0.364527	1.529	0.364484	1.685779	DDIT4	Lung	GTEx_v6	T	C	73762673	10	rs2219837	-0.05213	0.442125	ENSG00000168209.4
rs3180	Uterus_ENSG00000198246.7	20	0.038604	-4.159	0.364912	4.589829	SLC29A3	Uterus	GTEx_v6	T	C	73762673	10	rs2219837	0.141808	0.437369	ENSG00000198246.7
rs3180	Thyroid_ENSG00000227382.1	1	NA	5.270	0.365107	5.819052	EIF4A2P2	Thyroid	GTEx_v6	C	G	74046191	10	rs1074039	0.088012	0.458792	ENSG00000227382.1
rs3180	Brain cerebellar hemisphere_	6	0.396668	5.055	0.366239	5.595196	NUDT13	Brain cereb; GTEx_v6	G	A	73883196	10	rs1245578	-0.09403	0.448371	ENSG00000166321.9	
rs3180	Pancreas_ENSG00000107738.	20	0.37582	-1.693	0.367153	1.877639	C10orf54	Pancreas	GTEx_v6	T	C	73762673	10	rs2219837	0.057741	0.437652	ENSG00000107738.15
rs3180	Prostate_ENSG00000107731.!	20	0.517363	2.063	0.367399	2.289085	UNC5B	Prostate	GTEx_v6	T	C	73762673	10	rs2219837	-0.07036	0.435747	ENSG00000107731.8
rs3180	Esophagus gastroesophageal	20	0.88717	2.821	0.367874	3.132314	UNC5B	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	-0.09618	0.43663	ENSG00000107731.8
rs3180	Colon transverse_ENSG00000	1	NA	-3.464	0.368057	3.848708	FAM149B1	Colon tran	GTEx_v6	C	G	74046191	10	rs1074039	-0.05785	0.453891	ENSG00000138286.10
rs7814941	Brain putamen basal ganglia_	18	0.707091	0.783	0.368532	0.8706	FAM49B	Brain puta	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.034759	0.433045	ENSG00000153310.14
rs3180	Esophagus mucosa_ENSG000	16	0.036564	1.520	0.370115	1.695909	RPL17P50	Esophagus	GTEx_v6	A	G	73820622	10	rs3180	-0.05062	0.435156	ENSG00000213700.3
rs7814941	Cells EBV-transformed lympho	19	0.332293	-1.963	0.370894	2.193895	ASAP1	Cells EBV-t	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.08716	0.43172	ENSG00000153317.10
rs3180	Whole blood_ENSG00000227:	1	NA	4.396	0.371357	4.917672	EIF4A2P2	Whole blo	GTEx_v6	C	G	74046191	10	rs1074039	0.073414	0.450657	ENSG00000227382.1
rs7814941	Adipose visceral omentum_E	20	0.583842	1.258	0.372963	1.412016	ASAP1	Adipose vi	GTEx_v6	A	G	1.31E+08	8	rs1095648	0.055856	0.43031	ENSG00000153317.10
rs3180	Esophagus gastroesophageal	1	NA	5.968	0.373097	6.700053	DNAJC9	Esophagus	GTEx_v6	C	G	74046191	10	rs1074039	0.09966	0.446694	ENSG00000213551.4
rs3180	Nerve tibial_ENSG000001821	1	NA	2.415	0.374252	2.717494	MRPS16	Nerve tibi; GTEx_v6	C	G	74046191	10	rs1074039	0.040324	0.446487	ENSG00000182180.9	
rs3180	Vagina_ENSG00000221164.1	5	0.037649	8.204	0.375419	9.255604	SNORA11	Vagina	GTEx_v6	C	T	73899093	10	rs1245515	-0.15259	0.436136	ENSG00000221164.1
rs3180	Heart atrial appendage_ENS	20	0.193058	2.042	0.375749	2.30515	DDIT4	Heart atria	GTEx_v6	T	C	73762673	10	rs2219837	-0.06963	0.427587	ENSG00000168209.4
rs3180	Brain frontal cortex_BA9_EN	20	0.998224	2.112	0.376197	2.386925	ANAPC16	Brain front	GTEx_v6	T	C	73762673	10	rs2219837	-0.07203	0.425552	ENSG00000166295.4
rs3180	Artery tibial_ENSG000001821	1	NA	2.101	0.376617	2.37667	MRPS16	Artery tibi; GTEx_v6	C	G	74046191	10	rs1074039	0.035092	0.443542	ENSG00000182180.9	
rs3180	Brain cortex_ENSG000001228	1	NA	5.111	0.376704	5.781379	ECD	Brain corte	GTEx_v6	C	G	74046191	10	rs1074039	0.085348	0.440942	ENSG00000122882.6
rs7814941	Esophagus gastroesophageal	19	0.834953	-2.620	0.37695	2.965172	RP11-473C	Esophagus	GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.11632	0.424937	ENSG00000254317.1
rs3180	Colon transverse_ENSG00000	20	0.9658	-3.032	0.377646	3.436525	C10orf105	Colon tran	GTEx_v6	T	C	73762673	10	rs2219837	0.103386	0.425513	ENSG00000214688.4
rs3180	Brain caudate basal ganglia_E	20	0.642027	4.794	0.377824	5.435494	RP11-150C	Brain caud	GTEx_v6	T	C	73762673	10	rs2219837	-0.16346	0.424014	ENSG00000272988.1
rs3180	Ovary_ENSG00000198246.7	20	0.60197	-3.083	0.377993	3.497474	SLC29A3	Ovary	GTEx_v6	T	C	73762673	10	rs2219837	0.105143	0.42313	ENSG00000198246.7
rs12310519	Vagina_ENSG00000134532.11	11	0.521953	-1.471	0.37908	1.67247	SOX5	Vagina	GTEx_v6	C	T	23982559	12	rs9804988	0.085176	0.420194	ENSG00000134532.11
rs3180	Adipose visceral omentum_E	20	0.099271	2.207	0.379185	2.510148	C10orf105	Adipose vi	GTEx_v6	T	C	73762673	10	rs2219837	-0.07527	0.423909	ENSG00000214688.4
rs3180	Skin sun exposed lower leg_EI	20	0.252995	1.162	0.379228	1.321554	UNC5B	Skin sun e	GTEx_v6	T	C	73762673	10	rs2219837	-0.03963	0.424571	ENSG00000107731.8
rs12310519	Adipose subcutaneous_ENSG	11	0.509934	1.491	0.379506	1.697119	RP11-444L	Adipose su	GTEx_v6	C	T	23982559	12	rs9804988	-0.08635	0.422936	ENSG00000255864.1
rs3180	Whole blood_ENSG00000166:	20	0.186608	-1.090	0.380816	1.243383	ANAPC16	Whole blo	GTEx_v6	T	C	73762673	10	rs2219837	0.037159	0.422827	ENSG00000166295.4
rs12310519	Skin not sun exposed suprapu	11	0.238125	-1.303	0.381719	1.489055	SOX5	Skin not su	GTEx_v6	C	T	23982559	12	rs9804988	0.075416	0.419795	ENSG00000134532.11
rs12310519	Artery tibial_ENSG000001345	11	0.954373	-1.005	0.381783	1.149371	SOX5	Artery tibi; GTEx_v6	C	T	23982559	12	rs9804988	0.058204	0.420246	ENSG00000134532.11	
rs3180	Artery aorta_ENSG000001383	20	0.008287	-1.559	0.382982	1.786782	ASCC1	Artery aor	GTEx_v6	T	C	73762673	10	rs2219837	0.053156	0.419612	ENSG00000138303.13
rs3180	Cells transformed fibroblasts_	6	0.025659	-2.748	0.38337	3.152666	NUDT13	Cells trans	GTEx_v6	G	A	73883196	10	rs1245578	-0.051116	0.429553	ENSG00000166321.9
rs3180	Esophagus mucosa_ENSG000	20	0.081364	1.277	0.383739	1.465983	ASCC1	Esophagus	GTEx_v6	T	C	73762673	10	rs2219837	-0.04354	0.419059	ENSG00000138303.13
rs3180	Liver_ENSG00000198246.7	20	0.442537	2.723	0.383989	3.12818	SLC29A3	Liver	GTEx_v6	T	C	73762673	10	rs2219837	-0.09286	0.41676	ENSG00000198246.7
rs3180	Prostate_ENSG00000107745:	20	0.241353	-2.718	0.384241	3.123218	MICU1	Prostate	GTEx_v6	T	C	73762673	10	rs2219837	0.092668	0.416038	ENSG00000107745.12
rs3180	Liver_ENSG00000272599.1	5	0.277048	-6.119	0.384956	7.042958	RP11-152N	Liver	GTEx_v6	C	T	73899093	10	rs1245515	0.113812	0.42537	ENSG00000272599.1
rs3180	Pituitary_ENSG00000107742:	20	0.949091	-3.236	0.385512	3.728781	SPOCK2	Pituitary	GTEx_v6	T	C	73762673	10	rs2219837	0.11034	0.414536	ENSG00000107742.8
rs3180	Artery coronary_ENSG000002	5	0.026916	5.768	0.385529	6.647311	RP11-152N	Artery coro	GTEx_v6	C	T	73899093	10	rs1245515	-0.10729	0.425391	ENSG00000272599.1
rs3180	Spleen_ENSG00000213700.3	16	0.749805	-3.081	0.386795	3.559487	RPL17P50	Spleen	GTEx_v6	A	G	73820622	10	rs3180	0.102582	0.413205	ENSG00000213700.3
rs3180	Prostate_ENSG00000236756.~	1	NA	5.357	0.387667	6.201554	DNAJC9-A	Prostate	GTEx_v6	C	G	74046191	10	rs1074039	0.089466	0.426641	ENSG00000236756.4
rs3180	Vagina_ENSG00000198246.7	20	0.169407	-2.713	0.387723	3.141033	SLC29A3	Vagina	GTEx_v6	T	C	73762673	10	rs2219837	0.092516	0.411589	ENSG000000198246.7
rs3180	Lung_ENSG00000230526.1	20	0.888284	-2.231	0.390128	2.5956	RP11-472C	Lung	GTEx_v6	T	C	73762673	10	rs2219837	0.076064	0.411883	ENSG00000230526.1
rs3180	Skin sun exposed lower leg_EI	20	0.750137	0.882	0.390374	1.026781	ANAPC16	Skin sun e	GTEx_v6	T	C	73762673	10	rs2219837	-0.03007	0.411692	ENSG00000166295.4

rs3180	Stomach_ENSG00000214688.	20	0.917305	2.823	0.391211	3.292446	C10orf105	Stomach	GTEEx_v6	T	C	73762673	10	rs2219837	-0.09626	0.409894	ENSG00000214688.4
rs7814941	Lung_ENSG00000153317.10	20	0.463916	0.920	0.391262	1.072706	ASAP1	Lung	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.040833	0.409772	ENSG00000153317.10
rs3180	Brain cerebellar hemisphere_	5	0.043971	-7.058	0.391338	8.233604	RP11-152B	Brain cere	GTEEx_v6	C	T	73899093	10	rs1245515	0.131275	0.417302	ENSG00000272599.1
rs3180	Lung_ENSG00000122882.6	1	NA	-2.180	0.391706	2.54523	ECD	Lung	GTEEx_v6	C	G	74046191	10	rs1074039	-0.03641	0.424313	ENSG00000122882.6
rs3180	Brain caudate basal ganglia_E	6	0.193108	-6.143	0.391912	7.174676	NUDT13	Brain caud	GTEEx_v6	G	A	73883196	10	rs1245578	0.114253	0.417119	ENSG00000166321.9
rs7814941	Adipose visceral omentum_Et	20	0.894601	-0.926	0.394014	1.085906	FAM49B	Adipose vi	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.0411	0.406105	ENSG00000153310.14
rs3180	Muscle skeletal_ENSG000001	20	0.254239	-1.286	0.394257	1.509597	DDIT4	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	0.043855	0.407459	ENSG00000168209.4
rs3180	Esophagus gastroesophageal_j	1	NA	3.254	0.394629	3.823152	MRPS16	Esophagus	GTEEx_v6	C	G	74046191	10	rs1074039	0.05435	0.419423	ENSG00000182180.9
rs3180	Brain hippocampus_ENSG000	20	0.149006	2.439	0.394883	2.867194	C10orf54	Brain hippoc	GTEEx_v6	T	C	73762673	10	rs2219837	-0.08318	0.403634	ENSG00000107738.15
rs12310519	Heart left ventricle_ENSG000	11	0.683045	1.818	0.394994	2.137828	SOX5	Heart left v	GTEEx_v6	C	T	23982559	12	rs9804988	-0.10529	0.404707	ENSG00000134532.11
rs3180	Brain putamen basal ganglia_	1	NA	-9.411	0.396193	11.09192	EIF4A2P2	Brain puta	GTEEx_v6	C	G	74046191	10	rs1074039	-0.15716	0.415817	ENSG00000227382.1
rs3180	Testis_ENSG00000166228.4	2	NA	2.746	0.396315	3.237848	PCBD1	Testis	GTEEx_v6	C	T	73646408	10	rs1437267	0.060146	0.415185	ENSG00000166228.4
rs3180	Nerve tibial_ENSG000002001	20	0.989202	2.396	0.397064	2.829105	Y_RNA	Nerve tibii	GTEEx_v6	T	C	73762673	10	rs2219837	-0.0817	0.403961	ENSG00000200170.1
rs12310519	Brain putamen basal ganglia_	11	0.992826	1.444	0.397244	1.705437	SOX5	Brain puta	GTEEx_v6	C	T	23982559	12	rs9804988	-0.08359	0.399963	ENSG00000134532.11
rs3180	Prostate_ENSG00000213700..	16	0.222176	-3.576	0.397538	4.226652	RPL17P50	Prostate	GTEEx_v6	A	G	73820622	10	rs3180	0.119076	0.401122	ENSG00000213700.3
rs3180	Thyroid_ENSG00000138286.1	1	NA	2.322	0.397569	2.745081	FAM149B1	Thyroid	GTEEx_v6	C	G	74046191	10	rs1074039	0.038782	0.417093	ENSG00000138286.10
rs3180	Heart atrial appendage_ENSG	20	0.58552	-2.576	0.397634	3.044892	CDH23	Heart atria	GTEEx_v6	T	C	73762673	10	rs2219837	0.087826	0.402537	ENSG00000107736.15
rs3180	Esophagus gastroesophageal_j	20	0.100355	1.583	0.399802	1.880093	ASCC1	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05398	0.399841	ENSG00000138303.13
rs3180	Nerve tibial_ENSG000001487	20	0.291101	1.386	0.400069	1.647	DNAJB12	Nerve tibii	GTEEx_v6	T	C	73762673	10	rs2219837	-0.04726	0.400617	ENSG00000148719.10
rs12310519	Brain nucleus accumbens basa	11	0.134691	1.264	0.400095	1.502715	SOX5	Brain nuck	GTEEx_v6	C	T	23982559	12	rs9804988	-0.07321	0.397415	ENSG00000134532.11
rs3180	Brain cortex_ENSG000002146	20	0.668543	-2.395	0.400354	2.84817	C10orf105	Brain cort	GTEEx_v6	T	C	73762673	10	rs2219837	0.081679	0.398357	ENSG00000214688.4
rs3180	Muscle skeletal_ENSG000001	20	0.017189	1.298	0.401433	1.546638	CDH23	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	-0.04425	0.399446	ENSG00000107736.15
rs3180	Brain cortex_ENSG000001077	20	0.123742	-1.995	0.402999	2.3853	C10orf54	Brain corte	GTEEx_v6	T	C	73762673	10	rs2219837	0.068022	0.395462	ENSG00000107738.15
rs3180	Esophagus mucosa_ENSG000	20	0.113582	-1.208	0.403887	1.447352	SPOCK2	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	0.041196	0.396354	ENSG00000107742.8
rs3180	Whole blood_ENSG000001077	20	0.619383	-2.060	0.404056	2.468709	UNC5B	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	0.070242	0.396501	ENSG00000107731.8
rs3180	Brain putamen basal ganglia_	20	0.884471	-3.830	0.404075	4.590178	DNAJB12	Brain puta	GTEEx_v6	T	C	73762673	10	rs2219837	0.130599	0.393614	ENSG00000148719.10
rs3180	Brain cortex_ENSG000002729	20	0.30444	4.580	0.404642	5.495232	RP11-150C	Brain cort	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15616	0.393675	ENSG00000272988.1
rs3180	Brain hippocampus_ENSG000	20	0.143579	2.344	0.405222	2.81599	SPOCK2	Brain hipp	GTEEx_v6	T	C	73762673	10	rs2219837	-0.07992	0.39231	ENSG00000107742.8
rs3180	Prostate_ENSG00000198246..	20	0.193847	-3.587	0.406581	4.322549	SLC29A3	Prostate	GTEEx_v6	T	C	73762673	10	rs2219837	0.12233	0.391225	ENSG00000198246.7
rs3180	Artery aorta_ENSG000001487	20	0.453597	1.621	0.407801	1.958287	DNAJB12	Artery aor	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05528	0.391796	ENSG00000148719.10
rs3180	Spleen_ENSG00000272988.1	20	0.483046	-3.423	0.408389	4.140671	RP11-150C	Spleen	GTEEx_v6	T	C	73762673	10	rs2219837	0.116732	0.38933	ENSG00000272988.1
rs3180	Nerve tibial_ENSG000001382	1	NA	2.210	0.40902	2.676943	FAM149B1	Nerve tibia	GTEEx_v6	C	G	74046191	10	rs1074039	0.036909	0.403258	ENSG00000138286.10
rs3180	Uterus_ENSG00000168209.4	20	0.376558	4.526	0.409065	5.48217	DDIT4	Uterus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.15433	0.387455	ENSG00000168209.4
rs3180	Whole blood_ENSG000001228	8	0.293246	1.547	0.409485	1.875088	P4HA1	Whole blo	GTEEx_v6	T	C	73858549	10	rs1668156	-0.02892	0.398603	ENSG00000122884.8
rs3180	Uterus_ENSG00000272599.1	5	0.011305	-7.143	0.41001	8.670001	RP11-152B	Uterus	GTEEx_v6	C	T	73899093	10	rs1245515	0.13286	0.394437	ENSG00000272599.1
rs3180	Breast mammary tissue_ENSG	2	NA	3.115	0.410047	3.781147	PCBD1	Breast mai	GTEEx_v6	C	T	73646408	10	rs1437267	0.068217	0.399335	ENSG00000166228.4
rs3180	Brain frontal cortex_BA9_ENS	2	NA	3.983	0.410187	4.836789	PCBD1	Brain front	GTEEx_v6	C	T	73646408	10	rs1437267	0.087237	0.397544	ENSG00000166228.4
rs7814941	Brain caudate basal ganglia_E	18	0.741644	-2.413	0.41082	2.933854	RP11-473C	Brain caud	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.10714	0.386454	ENSG00000254317.1
rs7814941	Brain nucleus accumbens basa	18	0.639979	2.652	0.413771	3.244326	RP11-473C	Brain nuck	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.117727	0.383069	ENSG00000254317.1
rs7814941	Whole blood_ENSG000001533	20	0.764406	0.354	0.414347	0.433601	FAM49B	Whole blo	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.015715	0.384653	ENSG00000153310.14
rs3180	Small intestine terminal ileum	20	0.446872	-4.115	0.414868	5.047314	C10orf105	Small intes	GTEEx_v6	T	C	73762673	10	rs2219837	0.140334	0.381763	ENSG00000214688.4
rs12310519	Brain cortex_ENSG000002558	11	0.716832	-2.871	0.415567	3.526606	RP11-444C	Brain cort	GTEEx_v6	C	T	23982559	12	rs9804988	0.166239	0.380989	ENSG00000255864.1
rs3180	Ovary_ENSG00000107736.15	20	0.083692	-3.066	0.415657	3.766734	CDH23	Ovary	GTEEx_v6	T	C	73762673	10	rs2219837	0.104552	0.381445	ENSG00000107736.15
rs3180	Prostate_ENSG00000272627..	20	0.393434	-4.209	0.415676	5.171004	RP11-354E	Prostate	GTEEx_v6	T	C	73762673	10	rs2219837	0.143524	0.381521	ENSG00000272627.1
rs3180	Liver_ENSG00000227540.1	1	NA	-5.407	0.415888	6.64636	RP11-152B	Liver	GTEEx_v6	C	G	74046191	10	rs1074039	-0.0903	0.393379	ENSG00000227540.1
rs3180	Brain putamen basal ganglia_	1	NA	6.059	0.416125	7.450839	DNAJC9-A'	Brain puta	GTEEx_v6	C	G	74046191	10	rs1074039	0.101181	0.392396	ENSG00000236756.4
rs3180	Artery aorta_ENSG000002367	1	NA	5.177	0.417087	6.379969	DNAJC9-A'	Artery aor	GTEEx_v6	C	G	74046191	10	rs1074039	0.08646	0.393521	ENSG00000236756.4
rs3180	Vagina_ENSG00000213700.3	16	0.906098	2.507	0.418627	3.099575	RPL17P50	Vagina	GTEEx_v6	A	G	73820622	10	rs3180	-0.08348	0.378021	ENSG00000213700.3
rs3180	Cells transformed fibroblasts_	1	NA	-3.622	0.418644	4.477777	DNAJC9-A'	Cells trans	GTEEx_v6	C	G	74046191	10	rs1074039	-0.06048	0.392137	ENSG00000236756.4
rs3180	Artery coronary_ENSG000001	1	NA	3.967	0.418666	4.905363	FAM149B1	Artery cori	GTEEx_v6	C	G	74046191	10	rs1074039	0.066252	0.390824	ENSG00000138286.10

rs3180	Esophagus gastroesophageal	20	0.684398	-2.048	0.418861	2.533784	C10orf54	Esophagus	GTEX_v6	T	C	73762673	10	rs2219837	0.069847	0.379303	ENSG00000107738.15
rs3180	Brain nucleus accumbens basa	20	0.38595	-4.536	0.419008	5.613137	RP11-354E	Brain nucle	GTEX_v6	T	C	73762673	10	rs2219837	0.154685	0.378235	ENSG00000272627.1
rs3180	Colon transverse_ENSG00000	16	0.25578	-1.650	0.420047	2.045697	RPL17P50	Colon tran	GTEX_v6	A	G	73820622	10	rs3180	0.054929	0.378466	ENSG00000213700.3
rs3180	Vagina_ENSG00000197746.9	20	0.090883	-1.794	0.421577	2.232663	PSAP	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	0.061188	0.37493	ENSG00000197746.9
rs3180	Artery aorta_ENSG000001977	20	0.24275	1.597	0.421842	1.988211	PSAP	Artery aor	GTEX_v6	T	C	73762673	10	rs2219837	-0.05446	0.376827	ENSG00000197746.9
rs3180	Thyroid_ENSG00000156026.1	20	0.704842	1.256	0.42193	1.563533	MCU	Thyroid	GTEX_v6	T	C	73762673	10	rs2219837	-0.04282	0.377135	ENSG00000156026.10
rs3180	Uterus_ENSG00000272630.1	8	0.918675	-8.170	0.424203	10.22288	RP11-344N	Uterus	GTEX_v6	T	C	73865131	10	rs1100017	0.151955	0.378775	ENSG00000272630.1
rs3180	Brain cerebellum_ENSG00000	20	0.194665	2.291	0.424639	2.869672	MICU1	Brain cere	GTEX_v6	T	C	73762673	10	rs2219837	-0.07813	0.372717	ENSG00000107745.12
rs3180	Brain nucleus accumbens basa	8	0.17897	3.666	0.425283	4.597641	P4HA1	Brain nucle	GTEX_v6	T	C	73858549	10	rs1668156	-0.06855	0.378755	ENSG00000122884.8
rs3180	Nerve tibial_ENSG000002726	8	0.434725	3.230	0.425865	4.055931	RP11-344N	Nerve tibi	GTEX_v6	T	C	73865131	10	rs1100017	-0.06007	0.380125	ENSG00000272630.1
rs7814941	Adipose visceral omentum_E	20	0.741679	1.555	0.426782	1.956511	GSDMC	Adipose vi	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.069036	0.370957	ENSG00000147697.4
rs3180	Prostate_ENSG00000272599.	5	0.184241	-5.616	0.427345	7.075018	RP11-152N	Prostate	GTEX_v6	C	T	73899093	10	rs1245515	0.104453	0.376426	ENSG00000272599.1
rs3180	Heart left ventricle_ENSG000	1	NA	5.423	0.428936	6.856312	EIF4A2P2	Heart left	GTEX_v6	C	G	74046191	10	rs1074039	0.090571	0.380063	ENSG00000227382.1
rs3180	Pituitary_ENSG00000156026..	20	0.16817	4.628	0.429456	5.857022	MCU	Pituitary	GTEX_v6	T	C	73762673	10	rs2219837	-0.15781	0.367185	ENSG00000156026.10
rs3180	Ovary_ENSG00000166295.4	20	0.821036	2.211	0.430093	2.802721	ANAPC16	Ovary	GTEX_v6	T	C	73762673	10	rs2219837	-0.07541	0.36649	ENSG00000166295.4
rs3180	Testis_ENSG00000168209.4	20	0.071277	1.246	0.430313	1.57989	DDIT4	Testis	GTEX_v6	T	C	73762673	10	rs2219837	-0.04249	0.36766	ENSG00000168209.4
rs3180	Colon transverse_ENSG00000	5	0.299086	-4.888	0.430327	6.197941	SNORA11	Colon tran	GTEX_v6	C	T	73899093	10	rs1245515	0.090915	0.374704	ENSG00000221164.1
rs3180	Brain caudate basal ganglia_E	20	0.304287	2.087	0.430965	2.6502	C10orf54	Brain caud	GTEX_v6	T	C	73762673	10	rs2219837	-0.07117	0.366132	ENSG00000107738.15
rs3180	Cells transformed fibroblasts_	20	0.875615	-0.548	0.432116	0.697163	PSAP	Cells trans	GTEX_v6	T	C	73762673	10	rs2219837	0.018676	0.366559	ENSG00000197746.9
rs3180	Adrenal gland_ENSG0000019..	20	0.799312	-1.639	0.43216	2.086932	PSAP	Adrenal gl	GTEX_v6	T	C	73762673	10	rs2219837	0.0559	0.365519	ENSG00000197746.9
rs3180	Lung_ENSG00000272630.1	8	0.828076	2.756	0.432563	3.511741	RP11-344N	Lung	GTEX_v6	T	C	73865131	10	rs1100017	-0.05126	0.372948	ENSG00000272630.1
rs3180	Brain hippocampus_ENSG000	20	0.135207	3.691	0.433608	4.71413	CDH23	Brain hippoc	GTEX_v6	T	C	73762673	10	rs2219837	-0.12587	0.362682	ENSG00000107736.15
rs3180	Artery coronary_ENSG000002	1	NA	6.668	0.433733	8.517488	EIF4A2P2	Artery coro	GTEX_v6	C	G	74046191	10	rs1074039	0.11135	0.374001	ENSG00000227382.1
rs3180	Adipose visceral omentum_E	20	0.025528	-1.342	0.438164	1.731146	ASCC1	Adipose vi	GTEX_v6	T	C	73762673	10	rs2219837	0.045767	0.35997	ENSG00000138303.13
rs3180	Prostate_ENSG00000107742..	20	0.153327	2.876	0.438799	3.714378	SPOCK2	Prostate	GTEX_v6	T	C	73762673	10	rs2219837	-0.09806	0.357805	ENSG00000107742.8
rs3180	Brain cerebellum_ENSG00000	20	0.406556	-3.148	0.439509	4.07218	SLC29A3	Brain cere	GTEX_v6	T	C	73762673	10	rs2219837	0.107343	0.357601	ENSG00000198246.7
rs3180	Brain cortex_ENSG000001077	20	0.253253	-2.324	0.439734	3.007213	SPOCK2	Brain corte	GTEX_v6	T	C	73762673	10	rs2219837	0.079231	0.357169	ENSG00000107742.8
rs3180	Cells transformed fibroblasts_	1	NA	-1.573	0.440731	2.039773	FAM149B1	Cells trans	GTEX_v6	C	G	74046191	10	rs1074039	-0.02626	0.367574	ENSG00000138286.10
rs3180	Brain putamen basal ganglia_	16	0.770754	-2.195	0.440789	2.847141	RPL17P50	Brain puta	GTEX_v6	A	G	73820622	10	rs3180	0.073085	0.355567	ENSG00000213700.3
rs3180	Adipose subcutaneous_ENSG0	20	0.704397	1.859	0.440865	2.412412	UNC5B-AS	Adipose su	GTEX_v6	T	C	73762673	10	rs2219837	-0.0634	0.357775	ENSG00000237512.2
rs3180	Colon sigmoid_ENSG0000027..	8	0.367078	-4.514	0.441551	5.865823	RP11-344N	Colon sign	GTEX_v6	T	C	73865131	10	rs1100017	0.083964	0.362363	ENSG00000272630.1
rs3180	Testis_ENSG00000215086.2	20	0.372349	-2.943	0.441817	3.826816	NPM1P24	Testis	GTEX_v6	T	C	73762673	10	rs2219837	0.100367	0.356036	ENSG00000215086.2
rs3180	Heart atrial appendage_ENSG	20	0.022903	2.331	0.442674	3.035977	SPOCK2	Heart atria	GTEX_v6	T	C	73762673	10	rs2219837	-0.07948	0.355196	ENSG00000107742.8
rs3180	Heart left ventricle_ENSG000	20	0.416829	-1.682	0.443675	2.196455	UNC5B	Heart left	GTEX_v6	T	C	73762673	10	rs2219837	0.057373	0.354497	ENSG00000107731.8
rs3180	Stomach_ENSG00000197746..	20	0.881867	1.635	0.444713	2.139262	PSAP	Stomach	GTEX_v6	T	C	73762673	10	rs2219837	-0.05575	0.353292	ENSG00000197746.9
rs3180	Esophagus gastroesophageal	1	NA	6.505	0.445045	8.517379	DNAJC9-A	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.108629	0.361799	ENSG00000236756.4
rs3180	Adrenal gland_ENSG00000138	1	NA	-4.083	0.445247	5.34925	FAM149B1	Adrenal gl	GTEX_v6	C	G	74046191	10	rs1074039	-0.06819	0.361756	ENSG00000138286.10
rs3180	Colon sigmoid_ENSG0000021..	1	NA	-4.111	0.445733	5.391681	DNAJC9	Colon sign	GTEX_v6	C	G	74046191	10	rs1074039	-0.06866	0.361206	ENSG00000213551.4
rs3180	Skin sun exposed lower leg_EI	20	0.438839	-1.106	0.445965	1.450921	C10orf54	Skin sun e	GTEX_v6	T	C	73762673	10	rs2219837	0.037709	0.352702	ENSG00000107738.15
rs12310519	Thyroid_ENSG00000134532.1	11	0.080571	1.078	0.446295	1.415587	SOX5	Thyroid	GTEX_v6	C	T	23982559	12	rs9804988	-0.06242	0.351521	ENSG00000134532.11
rs3180	Pancreas_ENSG00000236756..	1	NA	-5.020	0.446358	6.592062	DNAJC9-A	Pancreas	GTEX_v6	C	G	74046191	10	rs1074039	-0.08383	0.360705	ENSG00000236756.4
rs3180	Brain cerebellum_ENSG00000	20	0.058148	-1.959	0.447583	2.57988	ASCC1	Brain cere	GTEX_v6	T	C	73762673	10	rs2219837	0.066812	0.349617	ENSG00000138303.13
rs3180	Heart atrial appendage_ENSG	1	NA	-2.872	0.448365	3.788433	FAM149B1	Heart atria	GTEX_v6	C	G	74046191	10	rs1074039	-0.04797	0.358721	ENSG00000138286.10
rs3180	Ovary_ENSG00000107738.15	20	0.622126	2.452	0.448608	3.235453	C10orf54	Ovary	GTEX_v6	T	C	73762673	10	rs2219837	-0.0836	0.348046	ENSG00000107738.15
rs3180	Testis_ENSG00000227382.1	1	NA	-5.890	0.449663	7.790992	EIF4A2P2	Testis	GTEX_v6	C	G	74046191	10	rs1074039	-0.09836	0.357344	ENSG00000227382.1
rs3180	Uterus_ENSG00000237512.2	20	0.878279	4.098	0.450214	5.426787	UNC5B-AS	Uterus	GTEX_v6	T	C	73762673	10	rs2219837	-0.13973	0.345663	ENSG00000237512.2
rs7814941	Esophagus mucosa_ENSG000	20	0.350883	-1.679	0.450268	2.22335	RP11-473C	Esophagus	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.07453	0.347751	ENSG00000243402.1
rs3180	Esophagus mucosa_ENSG000	20	0.773682	1.051	0.45048	1.393907	ANAPC16	Esophagus	GTEX_v6	T	C	73762673	10	rs2219837	-0.03585	0.348068	ENSG00000166295.4
rs3180	Muscle skeletal_ENSG000001	20	0.763283	0.702	0.451051	0.931738	PSAP	Muscle ske	GTEX_v6	T	C	73762673	10	rs2219837	-0.02395	0.347815	ENSG00000197746.9
rs3180	Breast mammary tissue_ENSG	20	0.081799	1.343	0.451978	1.786198	ASCC1	Breast mai	GTEX_v6	T	C	73762673	10	rs2219837	-0.04581	0.34627	ENSG00000138303.13

rs3180	Colon sigmoid_ENSG00000023	20	0.527235	-3.149	0.45212	4.187828	UNC5B-AS	Colon sign	GTEX_v6	T	C	73762673	10	rs2219837	0.107373	0.345625	ENSG00000237512.2
rs3180	Uterus_ENSG00000138286.1C	1	NA	-4.825	0.452922	6.428792	FAM149B1	Uterus	GTEX_v6	C	G	74046191	10	rs1074039	-0.08058	0.351788	ENSG00000138286.10
rs12310519	Nerve tibial_ENSG0000025586	11	0.047833	-1.373	0.453077	1.83017	RP11-444C	Nerve tibi	GTEX_v6	C	T	23982559	12	rs9804988	0.079507	0.344824	ENSG00000255864.1
rs3180	Stomach_gastroesophageal	5	0.063339	4.438	0.453608	5.922074	SNORA11	Stomach	GTEX_v6	C	T	73899093	10	rs1245515	-0.08255	0.350355	ENSG00000221164.1
rs3180	Esophagus_gastroesophageal	20	0.847502	1.867	0.454668	2.497142	CDH23	Esophagus	GTEX_v6	T	C	73762673	10	rs2219837	-0.06366	0.343203	ENSG00000107736.15
rs3180	Artery aorta_ENSG000002725	5	0.770075	3.949	0.454949	5.285042	RP11-152N	Artery aor	GTEX_v6	C	T	73899093	10	rs1245515	-0.07345	0.349216	ENSG00000272599.1
rs3180	Brain cortex_ENSG000001663	6	0.332047	5.276	0.4552	7.064415	NUDT13	Brain cort	GTEX_v6	G	A	73883196	10	rs1245578	-0.09812	0.347704	ENSG00000166321.9
rs3180	Adipose visceral omentum_EI	1	NA	-3.037	0.455417	4.068999	ECD	Adipose vi	GTEX_v6	C	G	74046191	10	rs1074039	-0.05072	0.351616	ENSG00000122882.6
rs3180	Brain hypothalamus_ENSG00	1	NA	5.459	0.455656	7.318055	RP11-152N	Brain hypc	GTEX_v6	C	G	74046191	10	rs1074039	0.091172	0.349584	ENSG00000227540.1
rs3180	Brain cortex_ENSG000002273	1	NA	-6.711	0.455669	8.995879	EIF4A2P2	Brain corte	GTEX_v6	C	G	74046191	10	rs1074039	-0.11207	0.35017	ENSG00000227382.1
rs3180	Brain cerebellum_ENSG0000	20	0.005919	1.774	0.456179	2.380619	C10orf54	Brain cere	GTEX_v6	T	C	73762673	10	rs2219837	-0.06049	0.341273	ENSG00000107738.15
rs3180	Brain putamen basal ganglia_	20	0.196468	-1.932	0.456461	2.594675	UNC5B	Brain puta	GTEX_v6	T	C	73762673	10	rs2219837	0.065889	0.340282	ENSG00000107731.8
rs3180	Muscle skeletal_ENSG000002	20	0.908269	1.798	0.456815	2.416891	NPM1P24	Muscle ske	GTEX_v6	T	C	73762673	10	rs2219837	-0.06133	0.342204	ENSG00000215086.2
rs7814941	Brain anterior cingulate corte	16	0.544803	3.914	0.456989	5.262358	RP11-473C	Brain ante	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.173791	0.338731	ENSG00000254317.1
rs3180	Skin sun exposed lower leg_EI	20	0.481832	-1.907	0.457112	2.56484	NPM1P24	Skin sun ex	GTEX_v6	T	C	73762673	10	rs2219837	0.065037	0.341797	ENSG00000215086.2
rs12310519	Esophagus_gastroesophageal	11	0.815493	-1.264	0.458644	1.706091	SOX5	Esophagus	GTEX_v6	C	T	23982559	12	rs9804988	0.073206	0.338667	ENSG00000134532.11
rs3180	Nerve tibial_ENSG000001560	20	0.858814	-1.043	0.458807	1.408174	MCU	Nerve tibi	GTEX_v6	T	C	73762673	10	rs2219837	0.035573	0.340026	ENSG00000156026.10
rs7814941	Stomach_ENSG00000254317.	20	0.922804	-2.250	0.459201	3.039768	RP11-473C	Stomach	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.0999	0.338685	ENSG00000254317.1
rs3180	Whole blood_ENSG00000213	1	NA	-2.116	0.45945	2.860221	DNAJC9	Whole blo	GTEX_v6	C	G	74046191	10	rs1074039	-0.03533	0.348044	ENSG00000213551.4
rs3180	Artery aorta_ENSG000001682	20	0.079191	-1.516	0.460486	2.05413	DDIT4	Artery aor	GTEX_v6	T	C	73762673	10	rs2219837	0.051697	0.338154	ENSG00000168209.4
rs3180	Artery aorta_ENSG000002135	1	NA	3.819	0.461559	5.186592	DNAJC9	Artery aor	GTEX_v6	C	G	74046191	10	rs1074039	0.063774	0.345393	ENSG00000213551.4
rs3180	Stomach_ENSG00000213700.	16	0.665206	1.520	0.462809	2.069738	RPL17P50	Stomach	GTEX_v6	A	G	73820622	10	rs3180	-0.0506	0.335747	ENSG00000213700.3
rs3180	Testis_ENSG00000122884.8	8	0.230157	2.752	0.46288	3.748434	P4HA1	Testis	GTEX_v6	T	C	73858549	10	rs1668156	-0.05146	0.340836	ENSG00000122884.8
rs3180	Testis_ENSG00000198246.7	20	0.118197	1.531	0.462962	2.085568	SLC29A3	Testis	GTEX_v6	T	C	73762673	10	rs2219837	-0.0522	0.335465	ENSG00000198246.7
rs3180	Brain anterior cingulate corte	1	NA	4.210	0.463435	5.741295	MRPS16	Brain ante	GTEX_v6	C	G	74046191	10	rs1074039	0.070299	0.341173	ENSG00000182180.9
rs3180	Pancreas_ENSG00000138303.	20	0.146258	1.000	0.463746	1.364572	ASCC1	Pancreas	GTEX_v6	T	C	73762673	10	rs2219837	-0.03409	0.334613	ENSG00000138303.13
rs3180	Brain caudate basal ganglia_E	20	0.324404	-2.141	0.464258	2.92479	C10orf105	Brain caud	GTEX_v6	T	C	73762673	10	rs2219837	0.072992	0.333503	ENSG00000214688.4
rs3180	Thyroid_ENSG00000227540.1	1	NA	-2.822	0.464757	3.860453	RP11-152N	Thyroid	GTEX_v6	C	G	74046191	10	rs1074039	-0.04713	0.342483	ENSG00000227540.1
rs3180	Brain frontal cortex BA9_ENS	20	0.02984	-4.299	0.465145	5.885969	RP11-150C	Brain front	GTEX_v6	T	C	73762673	10	rs2219837	0.1466	0.332431	ENSG00000272988.1
rs3180	Brain nucleus accumbens basa	1	NA	-5.510	0.465521	7.54979	RP11-152N	Brain nuck	GTEX_v6	C	G	74046191	10	rs1074039	-0.09201	0.34007	ENSG00000227540.1
rs7814941	Whole blood_ENSG00000253	20	0.379703	-1.347	0.46725	1.852606	RP11-473C	Whole blo	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.0598	0.331728	ENSG00000253720.1
rs3180	Cells transformed fibroblasts_	20	0.487281	1.644	0.468159	2.266366	NPM1P24	Cells trans	GTEX_v6	T	C	73762673	10	rs2219837	-0.05607	0.331179	ENSG00000215086.2
rs7814941	Thyroid_ENSG00000254317.1	20	0.536881	1.309	0.468286	1.805003	RP11-473C	Thyroid	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.058125	0.330618	ENSG00000254317.1
rs3180	Cells transformed fibroblasts_	20	0.083838	0.897	0.468471	1.236773	ASCC1	Cells trans	GTEX_v6	T	C	73762673	10	rs2219837	-0.03057	0.330885	ENSG00000138303.13
rs3180	Pancreas_ENSG00000213551.	1	NA	-3.833	0.469012	5.293215	DNAJC9	Pancreas	GTEX_v6	C	G	74046191	10	rs1074039	-0.06401	0.337427	ENSG00000213551.4
rs3180	Vagina_ENSG00000166295.4	20	0.528286	2.072	0.470114	2.868265	ANAPC16	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	-0.07065	0.327322	ENSG00000166295.4
rs7814941	Cells transformed fibroblasts_	20	0.760981	-0.558	0.470232	0.772317	FAM49B	Cells trans	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.02476	0.328779	ENSG00000153310.14
rs3180	Colon transverse_ENSG0000	2	NA	-2.672	0.470602	3.703065	PCBD1	Colon tran	GTEX_v6	C	T	73646408	10	rs1437267	-0.05851	0.334684	ENSG00000166228.4
rs3180	Brain hypothalamus_ENSG00	20	0.013815	3.191	0.471037	4.427183	DDIT4	Brain hypc	GTEX_v6	T	C	73762673	10	rs2219837	-0.10882	0.326513	ENSG00000168209.4
rs3180	Brain putamen basal ganglia_	8	0.544447	3.290	0.471672	4.57126	P4HA1	Brain puta	GTEX_v6	T	C	73858549	10	rs1668156	-0.06153	0.330875	ENSG00000122884.8
rs7814941	Lung_ENSG00000254317.1	20	0.926555	-1.004	0.472274	1.397191	RP11-473C	Lung	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.04459	0.326893	ENSG00000254317.1
rs3180	Lung_ENSG00000272599.1	5	0.05225	2.806	0.473001	3.910609	RP11-152N	Lung	GTEX_v6	C	T	73899093	10	rs1245515	-0.0522	0.331642	ENSG00000272599.1
rs3180	Brain frontal cortex BA9_ENS	8	0.870704	-5.483	0.473016	7.641193	RP11-344N	Brain front	GTEX_v6	T	C	73865131	10	rs1100017	0.101987	0.330034	ENSG00000272630.1
rs3180	Brain hippocampus_ENSG00	20	0.539447	4.388	0.473285	6.119176	RP11-150C	Brain hippoc	GTEX_v6	T	C	73762673	10	rs2219837	-0.14964	0.324432	ENSG00000272988.1
rs3180	Breast mammary tissue_ENS	1	NA	-4.641	0.473568	6.475932	EIF4A2P2	Breast mai	GTEX_v6	C	G	74046191	10	rs1074039	-0.07751	0.333239	ENSG00000227382.1
rs3180	Liver_ENSG00000168209.4	20	0.279633	2.942	0.474253	4.111529	DDIT4	Liver	GTEX_v6	T	C	73762673	10	rs2219837	-0.10033	0.324096	ENSG00000168209.4
rs3180	Cells EBV-transformed lympho	2	NA	-3.251	0.475066	4.550938	PCBD1	Cells EBV-t	GTEX_v6	C	T	73646408	10	rs1437267	-0.07119	0.329794	ENSG00000166228.4
rs3180	Thyroid_ENSG00000122884.8	8	0.194183	1.468	0.475291	2.056747	P4HA1	Thyroid	GTEX_v6	T	C	73858549	10	rs1668156	-0.02746	0.329345	ENSG00000122884.8
rs12310519	Esophagus muscularis_ENSG0	11	0.903358	-1.227	0.475311	1.718131	SOX5	Esophagus	GTEX_v6	C	T	23982559	12	rs9804988	0.071015	0.323688	ENSG00000134532.11
rs3180	Artery aorta_ENSG000001077	20	0.501573	1.389	0.476715	1.951319	MICU1	Artery aor	GTEX_v6	T	C	73762673	10	rs2219837	-0.04735	0.322906	ENSG00000107745.12

rs3180	Brain cerebellar hemisphere_	1 NA	3.880	0.476868	5.454944 ECD	Brain cerebellar hemisphere_	GTEEx_v6	C	G	74046191	10 rs1074039	0.064802	0.328718	ENSG00000122882.6
rs3180	Adipose visceral omentum_EI	20 0.750142	-1.331	0.477139	1.871583 CHST3	Adipose viscerale	GTEEx_v6	T	C	73762673	10 rs2219837	0.045371	0.322439	ENSG00000122863.5
rs3180	Esophagus muscularis_ENSG0	16 0.156533	-1.326	0.478144	1.869219 RPL17P50	Esophagus muscularis	GTEEx_v6	A	G	73820622	10 rs3180	0.04415	0.321712	ENSG00000213700.3
rs3180	Pituitary_ENSG0000148719.	20 0.757691	3.766	0.478882	5.318247 DNAJB12	Pituitary	GTEEx_v6	T	C	73762673	10 rs2219837	-0.12842	0.319539	ENSG00000148719.10
rs3180	Small intestine terminal ileum	1 NA	4.614	0.47899	6.517543 DNAJC9	Small intestine terminal ileum	GTEEx_v6	C	G	74046191	10 rs1074039	0.077053	0.326153	ENSG00000213551.4
rs3180	Esophagus mucosa_ENSG0000	5 0.979794	-2.302	0.479874	3.258909 RP11-152N	Esophagus mucosa	GTEEx_v6	C	T	73899093	10 rs1245515	0.042825	0.324918	ENSG00000272599.1
rs3180	Whole blood_ENSG00000213	16 0.218755	0.917	0.480436	1.299791 RPL17P50	Whole blood	GTEEx_v6	A	G	73820622	10 rs3180	-0.03054	0.319928	ENSG00000213700.3
rs3180	Spleen_ENSG00000107736.15	20 0.124581	3.048	0.480442	4.32024 CDH23	Spleen	GTEEx_v6	T	C	73762673	10 rs2219837	-0.10395	0.318186	ENSG00000107736.15
rs3180	Prostate_ENSG00000156026.	20 0.648547	-2.289	0.480502	3.24484 MCU	Prostate	GTEEx_v6	T	C	73762673	10 rs2219837	0.078062	0.3181	ENSG00000156026.10
rs3180	Artery aorta_ENSG000001077	20 0.830921	-1.153	0.480505	1.633739 C10orf54	Artery aorta	GTEEx_v6	T	C	73762673	10 rs2219837	0.039303	0.319422	ENSG00000107738.15
rs3180	Pituitary_ENSG00000213700.	16 0.48763	-3.412	0.480801	4.839378 RPL17P50	Pituitary	GTEEx_v6	A	G	73820622	10 rs3180	0.113614	0.317804	ENSG00000213700.3
rs3180	Nerve tibial_ENSG000002273	1 NA	-4.322	0.480893	6.131385 EIF4A2P2	Nerve tibial	GTEEx_v6	C	G	74046191	10 rs1074039	-0.07217	0.326399	ENSG00000227382.1
rs3180	Brain cerebellar hemisphere_	20 0.777802	2.794	0.481848	3.973129 UNC5B	Brain cerebellar hemisphere_	GTEEx_v6	T	C	73762673	10 rs2219837	-0.09529	0.31691	ENSG00000107731.8
rs7814941	Cells transformed fibroblasts_	20 0.007652	0.941	0.482238	1.339509 GSDMC	Cells transformed fibroblasts_	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.041793	0.31771	ENSG00000147697.4
rs3180	Skin sun exposed lower leg_EI	20 0.621008	1.519	0.482317	2.162435 C10orf105	Skin sun exposed lower leg_EI	GTEEx_v6	T	C	73762673	10 rs2219837	-0.05181	0.318123	ENSG00000214688.4
rs7814941	Stomach_ENSG00000153310.	20 0.426953	-0.927	0.482434	1.319438 FAM49B	Stomach	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.04115	0.317063	ENSG00000153310.14
rs3180	Whole blood_ENSG00000200	20 0.603738	1.733	0.482583	2.46853 Y_RNA	Whole blood	GTEEx_v6	T	C	73762673	10 rs2219837	-0.05911	0.31795	ENSG00000200170.1
rs3180	Colon transverse_ENSG00000	1 NA	2.349	0.482638	3.34619 ECD	Colon transverse	GTEEx_v6	C	G	74046191	10 rs1074039	0.039232	0.324258	ENSG00000122882.6
rs3180	Adipose subcutaneous_ENSG0	1 NA	-1.477	0.48526	2.117106 MRPS16	Adipose subcutaneous	GTEEx_v6	C	G	74046191	10 rs1074039	-0.02467	0.32229	ENSG00000182180.9
rs3180	Small intestine terminal ileum	8 0.223945	-4.508	0.485597	6.464127 P4HA1	Small intestine terminal ileum	GTEEx_v6	T	C	73858549	10 rs1668156	0.084293	0.317442	ENSG00000122884.8
rs7814941	Brain nucleus accumbens bas	18 0.736071	-1.385	0.485829	1.986569 ASAP1	Brain nucleus accumbens basal	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.06147	0.313041	ENSG00000153317.10
rs3180	Brain cortex_ENSG000001662	2 NA	-3.082	0.48583	4.421713 PCBD1	Brain cortex	GTEEx_v6	C	T	73646408	10 rs1437267	-0.06749	0.31908	ENSG00000166228.4
rs3180	Small intestine terminal ileum	20 0.57931	2.972	0.486829	4.273734 C10orf54	Small intestine terminal ileum	GTEEx_v6	T	C	73762673	10 rs2219837	-0.10134	0.311949	ENSG00000107738.15
rs7814941	Whole blood_ENSG00000153	20 0.106678	0.505	0.488275	0.728389 ASAP1	Whole blood	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.022414	0.312391	ENSG00000153317.10
rs3180	Esophagus gastroesophageal j	6 0.250955	-3.524	0.488951	5.092238 NUDT13	Esophagus gastroesophageal junction	GTEEx_v6	G	A	73883196	10 rs1245578	0.065541	0.315661	ENSG00000166321.9
rs7814941	Esophagus gastroesophageal j	19 0.615735	1.944	0.491019	2.823218 ASAP1	Esophagus gastroesophageal junction	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.086328	0.309058	ENSG00000153317.10
rs7814941	Prostate_ENSG00000254317.	18 0.310202	2.086	0.491933	3.035101 RP11-473C	Prostate	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.092611	0.307455	ENSG000000254317.1
rs3180	Ovary_ENSG00000122863.5	20 0.65461	1.999	0.492174	2.909817 CHST3	Ovary	GTEEx_v6	T	C	73762673	10 rs2219837	-0.06815	0.307551	ENSG00000122863.5
rs3180	Brain cerebellum_ENSG00000	1 NA	-5.042	0.492885	7.353046 RP11-152N	Brain cerebellum	GTEEx_v6	C	G	74046191	10 rs1074039	-0.0842	0.313788	ENSG00000227540.1
rs3180	Liver_ENSG00000272630.1	8 0.523039	-4.918	0.493576	7.183218 RP11-344N	Liver	GTEEx_v6	T	C	73865131	10 rs1100017	0.091472	0.31083	ENSG00000272630.1
rs3180	Brain cerebellum_ENSG00000	20 0.215781	1.995	0.493831	2.91638 DDIT4	Brain cerebellum	GTEEx_v6	T	C	73762673	10 rs2219837	-0.06805	0.306542	ENSG00000168209.4
rs3180	Colon transverse_ENSG00000	20 0.038579	-1.173	0.494597	1.717592 ASCC1	Colon transverse	GTEEx_v6	T	C	73762673	10 rs2219837	0.040004	0.306529	ENSG00000138303.13
rs3180	Colon sigmoid_ENSG0000022	1 NA	-4.543	0.494869	6.655498 RP11-152N	Colon sigmoid	GTEEx_v6	C	G	74046191	10 rs1074039	-0.07587	0.312295	ENSG00000227540.1
rs3180	Spleen_ENSG00000122863.5	20 0.667652	2.390	0.494982	3.501656 CHST3	Spleen	GTEEx_v6	T	C	73762673	10 rs2219837	-0.08148	0.305166	ENSG00000122863.5
rs3180	Testis_ENSG00000236756.4	1 NA	-2.965	0.495352	4.34807 DNAJC9-A	Testis	GTEEx_v6	C	G	74046191	10 rs1074039	-0.04951	0.312062	ENSG00000236756.4
rs3180	Breast mammary tissue_ENSG	20 0.769801	-1.200	0.496139	1.763088 C10orf54	Breast mammary tissue	GTEEx_v6	T	C	73762673	10 rs2219837	0.040917	0.305263	ENSG00000107738.15
rs3180	Stomach_ENSG00000227540.	1 NA	3.305	0.496904	4.864673 RP11-152N	Stomach	GTEEx_v6	C	G	74046191	10 rs1074039	0.055192	0.310717	ENSG00000227540.1
rs3180	Testis_ENSG00000213551.4	1 NA	-3.637	0.497824	5.365056 DNAJC9	Testis	GTEEx_v6	C	G	74046191	10 rs1074039	-0.06074	0.309753	ENSG00000213551.4
rs3180	Brain frontal cortex BA9_ENS	20 0.032733	2.095	0.498532	3.095701 DDIT4	Brain frontal cortex BA9	GTEEx_v6	T	C	73762673	10 rs2219837	-0.07145	0.302133	ENSG00000168209.4
rs3180	Thyroid_ENSG00000237512.2	20 0.265287	1.761	0.498929	2.60457 UNC5B-AS	Thyroid	GTEEx_v6	T	C	73762673	10 rs2219837	-0.06006	0.303158	ENSG00000237512.2
rs3180	Vagina_ENSG00000236756.4	1 NA	-6.365	0.499295	9.421399 DNAJC9-A	Vagina	GTEEx_v6	C	G	74046191	10 rs1074039	-0.1063	0.307125	ENSG00000236756.4
rs3180	Adrenal gland_ENSG0000023	20 0.81733	-2.139	0.499428	3.166384 UNC5B-AS	Adrenal gland	GTEEx_v6	T	C	73762673	10 rs2219837	0.072924	0.301983	ENSG00000237512.2
rs3180	Pancreas_ENSG00000200170.	20 0.494675	2.228	0.499721	3.301222 Y_RNA	Pancreas	GTEEx_v6	T	C	73762673	10 rs2219837	-0.07598	0.301821	ENSG00000200170.1
rs3180	Brain caudate basal ganglia_E	20 0.098174	1.865	0.500665	2.768872 SPOCK2	Brain caudate basal ganglia	GTEEx_v6	T	C	73762673	10 rs2219837	-0.06359	0.300467	ENSG00000107742.8
rs3180	Muscle skeletal_ENSG000002	5 0.156014	-2.344	0.501978	3.491389 RP11-152N	Muscle skeletal	GTEEx_v6	C	T	73899093	10 rs1245515	0.043599	0.30458	ENSG00000272599.1
rs3180	Brain putamen basal ganglia_	1 NA	-6.065	0.502111	9.036302 RP11-152N	Brain putamen basal ganglia	GTEEx_v6	C	G	74046191	10 rs1074039	-0.10128	0.304614	ENSG00000227540.1
rs3180	Brain cerebellar hemisphere_	20 0.249929	2.342	0.502447	3.492649 MICU1	Brain cerebellar hemisphere	GTEEx_v6	T	C	73762673	10 rs2219837	-0.07987	0.298632	ENSG00000107745.12
rs3180	Stomach_ENSG00000237512.	20 0.701783	1.689	0.502832	2.520525 UNC5B-AS	Stomach	GTEEx_v6	T	C	73762673	10 rs2219837	-0.05759	0.299288	ENSG000000237512.2
rs3180	Whole blood_ENSG00000272	20 0.568387	-1.614	0.503574	2.41261 RP11-150C	Whole blood	GTEEx_v6	T	C	73762673	10 rs2219837	0.055029	0.299197	ENSG000000272988.1
rs12310519	Brain nucleus accumbens bas	11 0.096581	-2.546	0.504195	3.812588 RP11-444C	Brain nucleus accumbens basal	GTEEx_v6	C	T	23982559	12 rs9804988	0.147439	0.296733	ENSG00000255864.1

rs3180	Colon sigmoid_ENSG00000021:	16	0.676018	1.746	0.506053	2.625085	RPL17P50	Colon sign GTEx_v6	A	G	73820622	10	rs3180	-0.05813	0.296196	ENSG00000213700.3
rs7814941	Esophagus mucosa_ENSG0000	20	0.525927	0.550	0.50619	0.827766	FAM49B	Esophagus GTEx_v6	A	G	1.31E+08	8	rs1095648	0.024433	0.296376	ENSG00000153310.14
rs3180	Brain cortex_ENSG000001077	20	0.529115	-1.845	0.50732	2.782092	MICU1	Brain corte GTEx_v6	T	C	73762673	10	rs2219837	0.0629	0.294604	ENSG00000107745.12
rs3180	Vagina_ENSG00000107738.15	20	0.300875	-2.826	0.507587	4.264977	C10orf54	Vagina GTEx_v6	T	C	73762673	10	rs2219837	0.096366	0.293888	ENSG00000107738.15
rs3180	Stomach_ENSG00000272599.	5	0.6997	3.033	0.507672	4.578485	RP11-152	Stomach GTEx_v6	C	T	73899093	10	rs1245515	-0.05642	0.298849	ENSG00000272599.1
rs3180	Brain cortex_ENSG000001982	20	0.466525	-2.526	0.508439	3.820454	SLC29A3	Brain corte GTEx_v6	T	C	73762673	10	rs2219837	0.086149	0.293642	ENSG00000198246.7
rs7814941	Adrenal gland_ENSG0000015:	19	0.335462	-1.481	0.50929	2.244258	FAM49B	Adrenal gli GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.06576	0.293088	ENSG00000153310.14
rs3180	Stomach_ENSG00000138315.	20	0.64101	2.166	0.511027	3.295816	OIT3	Stomach GTEx_v6	T	C	73762673	10	rs2219837	-0.07387	0.292197	ENSG00000138315.8
rs3180	Adipose visceral omentum_E	20	0.136881	1.116	0.511108	1.69782	DNAJB12	Adipose vi GTEx_v6	T	C	73762673	10	rs2219837	-0.03804	0.292225	ENSG00000148719.10
rs3180	Colon transverse_ENSG0000	5	0.350098	-3.150	0.511326	4.795991	RP11-152	Colon tran GTEx_v6	C	T	73899093	10	rs1245515	0.058588	0.295584	ENSG00000272599.1
rs3180	Brain frontal cortex_BA9_ENS	20	0.197124	2.738	0.511775	4.174045	SLC29A3	Brain front GTEx_v6	T	C	73762673	10	rs2219837	-0.09338	0.290686	ENSG00000198246.7
rs3180	Cells transformed fibroblasts_	16	0.335308	0.629	0.511965	0.959458	RPL17P50	Cells trans GTEx_v6	A	G	73820622	10	rs3180	-0.02095	0.291809	ENSG00000213700.3
rs3180	Breast mammary tissue_ENSG	8	0.912529	2.893	0.513504	4.427971	RP11-344	Breast mai GTEx_v6	T	C	73865131	10	rs1100017	-0.05381	0.293751	ENSG00000272630.1
rs3180	Stomach_ENSG00000107742.	20	0.645438	1.494	0.513859	2.289033	SPOCK2	Stomach GTEx_v6	T	C	73762673	10	rs2219837	-0.05096	0.289774	ENSG00000107742.8
rs3180	Uterus_ENSG00000272627.1	20	0.864805	-3.167	0.51422	4.855864	RP11-354	E Uterus GTEx_v6	T	C	73762673	10	rs2219837	0.108008	0.287834	ENSG00000272627.1
rs3180	Testis_ENSG00000259267.1	4	0.580299	-3.648	0.514475	5.596036	RP11-432	J Testis GTEx_v6	C	T	73646408	10	rs1437267	-0.07989	0.293578	ENSG00000259267.1
rs3180	Brain cerebellar hemisphere_	1	NA	-6.150	0.514518	9.434396	DNAJC9-A	Brain cerel GTEx_v6	C	G	74046191	10	rs1074039	-0.1027	0.293632	ENSG00000236756.4
rs3180	Whole blood_ENSG00000107	20	0.176808	1.038	0.514803	1.593721	CDH23	Whole blo GTEx_v6	T	C	73762673	10	rs2219837	-0.0354	0.289495	ENSG00000107736.15
rs3180	Brain hypothalamus_ENSG00	20	0.948264	4.604	0.514837	7.068828	RP11-150	C Brain hypc GTEx_v6	T	C	73762673	10	rs2219837	-0.157	0.287748	ENSG00000272988.1
rs3180	Lung_ENSG00000221164.1	5	0.863084	3.161	0.515191	4.857977	SNORA11	Lung GTEx_v6	C	T	73899093	10	rs1245515	-0.0588	0.2926	ENSG00000221164.1
rs3180	Uterus_ENSG00000227540.1	1	NA	5.877	0.515312	9.033449	RP11-152	N Uterus GTEx_v6	C	G	74046191	10	rs1074039	0.098147	0.292217	ENSG00000227540.1
rs3180	Ovary_ENSG00000168209.4	20	0.401165	-2.064	0.51605	3.178711	DDIT4	Ovary GTEx_v6	T	C	73762673	10	rs2219837	0.070396	0.286888	ENSG00000168209.4
rs3180	Brain cortex_ENSG000001383	20	0.010193	1.568	0.516198	2.414892	ASCC1	Brain corte GTEx_v6	T	C	73762673	10	rs2219837	-0.05346	0.287029	ENSG00000138303.13
rs3180	Adipose subcutaneous_ENSG	20	0.602792	1.417	0.516278	2.182856	OIT3	Adipose su GTEx_v6	T	C	73762673	10	rs2219837	-0.04832	0.288169	ENSG00000138315.8
rs7814941	Vagina_ENSG00000254317.1	17	0.77375	2.032	0.516283	3.130866	RP11-473	C Vagina GTEx_v6	A	G	1.31E+08	8	rs1095648	0.09023	0.286179	ENSG00000254317.1
rs3180	Brain putamen basal ganglia_	2	NA	-3.504	0.516998	5.406924	PCBD1	Brain puta GTEx_v6	C	T	73646408	10	rs1437267	-0.07673	0.290269	ENSG00000166228.4
rs3180	Brain frontal cortex_BA9_ENS	16	0.100221	1.594	0.517249	2.461891	RPL17P50	Brain front GTEx_v6	A	G	73820622	10	rs3180	-0.05309	0.286054	ENSG00000213700.3
rs3180	Vagina_ENSG00000122882.6	1	NA	-4.599	0.518503	7.123405	ECD	Vagina GTEx_v6	C	G	74046191	10	rs1074039	-0.07681	0.289801	ENSG00000122882.6
rs3180	Lung_ENSG00000107745.12	20	0.434961	-0.862	0.518898	1.335992	MICU1	Lung GTEx_v6	T	C	73762673	10	rs2219837	0.029387	0.285903	ENSG00000107745.12
rs3180	Breast mammary tissue_ENSG	1	NA	3.159	0.518911	4.897324	DNAJC9	Breast mai GTEx_v6	C	G	74046191	10	rs1074039	0.052754	0.290766	ENSG00000213551.4
rs3180	Pancreas_ENSG00000148719.	20	0.09091	1.102	0.520182	1.713345	DNAJB12	Pancreas GTEx_v6	T	C	73762673	10	rs2219837	-0.03757	0.284237	ENSG00000148719.10
rs3180	Artery tibial_ENSG000002275	1	NA	-2.193	0.520273	3.41075	RP11-152	N Artery tibi GTEx_v6	C	G	74046191	10	rs1074039	-0.03662	0.289905	ENSG00000227540.1
rs3180	Brain frontal cortex_BA9_ENS	20	0.248608	2.018	0.520957	3.144253	DNAJB12	Brain front GTEx_v6	T	C	73762673	10	rs2219837	-0.06882	0.282926	ENSG00000148719.10
rs3180	Artery aorta_ENSG000001662	2	NA	2.327	0.522339	3.637295	PCBD1	Artery aor GTEx_v6	C	T	73646408	10	rs1437267	0.05096	0.286905	ENSG00000166228.4
rs3180	Adipose subcutaneous_ENSG	1	NA	1.738	0.522744	2.719853	ECD	Adipose su GTEx_v6	C	G	74046191	10	rs1074039	0.02903	0.287745	ENSG00000122882.6
rs12310519	Stomach_ENSG00000134532.	11	0.99124	-0.818	0.523313	1.281832	SOX5	Stomach GTEx_v6	C	T	23982559	12	rs9804988	0.04737	0.281356	ENSG00000134532.11
rs3180	Spleen_ENSG00000227382.1	1	NA	7.552	0.523423	11.83486	EIF4A2P2	Spleen GTEx_v6	C	G	74046191	10	rs1074039	0.126111	0.285768	ENSG00000227382.1
rs3180	Artery coronary_ENSG000002	20	0.322425	-2.718	0.523861	4.264023	NPM1P24	Artery cor GTEx_v6	T	C	73762673	10	rs2219837	0.092681	0.280972	ENSG00000215086.2
rs3180	Whole blood_ENSG00000272	20	0.633819	-1.545	0.524295	2.426904	RP11-354	E Whole blo GTEx_v6	T	C	73762673	10	rs2219837	-0.052695	0.281463	ENSG00000272627.1
rs3180	Brain cerebellum_ENSG00000	20	0.095097	2.220	0.524475	3.488579	DNAJB12	Brain cerel GTEx_v6	T	C	73762673	10	rs2219837	-0.07571	0.280227	ENSG00000148719.10
rs3180	Brain cerebellar hemisphere_	1	NA	2.590	0.525026	4.075241	MRPS16	Brain cerel GTEx_v6	C	G	74046191	10	rs1074039	0.043258	0.284369	ENSG00000182180.9
rs3180	Cells transformed fibroblasts_	20	0.981258	-0.742	0.525268	1.168126	ANAPC16	Cells trans GTEx_v6	T	C	73762673	10	rs2219837	0.025304	0.28053	ENSG00000166295.4
rs7814941	Thyroid_ENSG00000153317.1	20	0.004621	0.839	0.52566	1.322353	ASAP1	Thyroid GTEx_v6	A	G	1.31E+08	8	rs1095648	0.037262	0.279927	ENSG00000153317.10
rs3180	Pancreas_ENSG00000107736.	20	0.281585	1.404	0.526675	2.218363	CDH23	Pancreas GTEx_v6	T	C	73762673	10	rs2219837	-0.04789	0.278806	ENSG00000107736.15
rs3180	Brain cerebellum_ENSG00000	1	NA	3.585	0.52709	5.668756	FAM149B1	Brain cerel GTEx_v6	C	G	74046191	10	rs1074039	0.059873	0.282891	ENSG00000138286.10
rs3180	Prostate_ENSG00000226701.	20	0.784809	3.578	0.527133	5.65713	RP11-570	C Prostate GTEx_v6	T	C	73762673	10	rs2219837	-0.12199	0.277684	ENSG00000226701.1
rs3180	Brain cerebellum_ENSG00000	20	0.084141	1.948	0.528551	3.091442	C10orf105	Brain cerel GTEx_v6	T	C	73762673	10	rs2219837	-0.06644	0.276845	ENSG00000214688.4
rs7814941	Uterus_ENSG00000153310.14	16	0.554788	1.832	0.528736	2.908987	FAM49B	Uterus GTEx_v6	A	G	1.31E+08	8	rs1095648	0.081362	0.275463	ENSG00000153310.14
rs3180	Thyroid_ENSG00000214688.4	20	0.037528	1.676	0.529328	2.664679	C10orf105	Thyroid GTEx_v6	T	C	73762673	10	rs2219837	-0.05716	0.277162	ENSG00000214688.4
rs3180	Cells transformed fibroblasts_	1	NA	-2.278	0.530324	3.630659	RP11-152	Cells trans GTEx_v6	C	G	74046191	10	rs1074039	-0.03805	0.281058	ENSG00000227540.1

rs3180	Uterus_ENSG00000227382.1	1 NA	-7.237	0.530456	11.53638	EIF4A2P2	Uterus	GTEEx_v6	C	G	74046191	10 rs1074039	-0.12086	0.279007	ENSG00000227382.1
rs3180	Artery aorta_ENSG000001383	20 0.384548	-2.188	0.530838	3.491843	OIT3	Artery aor <small>t</small>	GTEEx_v6	T	C	73762673	10 rs2219837	0.074626	0.275676	ENSG00000138315.8
rs3180	Heart atrial appendage_ENSG	2 NA	2.013	0.530859	3.212278	PCBD1	Heart atria	GTEEx_v6	C	T	73646408	10 rs1437267	0.044087	0.279292	ENSG00000166228.4
rs3180	Artery coronary_ENSG000001	1 NA	-1.913	0.532328	3.063705	MRPS16	Artery cor <i>t</i>	GTEEx_v6	C	G	74046191	10 rs1074039	-0.03195	0.278595	ENSG00000182180.9
rs3180	Brain caudate basal ganglia_E	16 0.895216	-1.696	0.533878	2.726024	RPL17P50	Brain caud	GTEEx_v6	A	G	73820622	10 rs3180	0.056472	0.272242	ENSG00000213700.3
rs3180	Nerve tibial_ENSG000001228	1 NA	-2.225	0.534745	3.584493	ECD	Nerve tibi	GTEEx_v6	C	G	74046191	10 rs1074039	-0.03716	0.277202	ENSG00000122882.6
rs7814941	Esophagus mucosa_ENSG000	20 0.735659	0.988	0.534817	1.592469	RP11-473C	Esophagus	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.043885	0.272287	ENSG00000254317.1
rs12310519	Spleen_ENSG00000134532.11	11 0.398367	-1.851	0.534898	2.983416	SOX5	Spleen	GTEEx_v6	C	T	23982559	12 rs9804988	0.107193	0.270951	ENSG00000134532.11
rs3180	Adipose subcutaneous_ENSG	20 0.289555	1.092	0.535661	1.762658	CDH23	Adipose su	GTEEx_v6	T	C	73762673	10 rs2219837	-0.03723	0.271978	ENSG00000107736.15
rs3180	Brain putamen basal ganglia_	5 0.484274	-5.989	0.536292	9.683744	RP11-152	Brain puta	GTEEx_v6	C	T	73899093	10 rs1245515	0.11139	0.272953	ENSG00000272599.1
rs12310519	Cells transformed fibroblasts_	11 0.172922	0.898	0.536484	1.453555	SOX5	Cells trans	GTEEx_v6	C	T	23982559	12 rs9804988	-0.05202	0.270871	ENSG00000134532.11
rs3180	Brain cortex_ENSG000001682	20 0.577559	1.790	0.537263	2.900883	DDIT4	Brain cort	GTEEx_v6	T	C	73762673	10 rs2219837	-0.06103	0.269575	ENSG00000168209.4
rs3180	Artery aorta_ENSG000001662	20 0.813643	-0.893	0.537372	1.448062	ANAPC16	Artery aor <small>t</small>	GTEEx_v6	T	C	73762673	10 rs2219837	0.030457	0.270312	ENSG00000166295.4
rs3180	Brain cerebellum_ENSG00000	1 NA	3.034	0.539759	4.947436	ECD	Brain cere	GTEEx_v6	C	G	74046191	10 rs1074039	0.050662	0.272032	ENSG00000122882.6
rs3180	Heart atrial appendage_ENSG	20 0.943016	-1.461	0.54111	2.38997	SLC29A3	Heart atria	GTEEx_v6	T	C	73762673	10 rs2219837	0.049808	0.267065	ENSG00000198246.7
rs3180	Artery aorta_ENSG000001077	20 0.328232	1.162	0.541452	1.903094	UNC5B	Artery aor <small>t</small>	GTEEx_v6	T	C	73762673	10 rs2219837	-0.03963	0.266997	ENSG00000107731.8
rs3180	Artery tibial_ENSG000002273	1 NA	-3.356	0.543132	5.518968	EIF4A2P2	Artery tibi	GTEEx_v6	C	G	74046191	10 rs1074039	-0.05605	0.270124	ENSG00000227382.1
rs3180	Muscle skeletal_ENSG000001	20 0.05119	0.724	0.543455	1.191951	MCU	Muscle ske	GTEEx_v6	T	C	73762673	10 rs2219837	-0.0247	0.265724	ENSG00000156026.10
rs3180	Brain caudate basal ganglia_E	20 0.326537	-1.520	0.543497	2.502451	ASCC1	Brain caud	GTEEx_v6	T	C	73762673	10 rs2219837	0.051843	0.26462	ENSG00000138303.13
rs3180	Esophagus muscularis_ENSG0	1 NA	-2.321	0.543921	3.824638	ECD	Esophagus	GTEEx_v6	C	G	74046191	10 rs1074039	-0.03876	0.269298	ENSG00000122882.6
rs7814941	Thyroid_ENSG00000243402.1	20 0.490547	-1.385	0.544489	2.284786	RP11-473C	Thyroid	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.06148	0.264521	ENSG00000243402.1
rs7814941	Brain cerebellum_ENSG00000	18 0.288015	-2.428	0.544814	4.010244	RP11-473C	Brain cere	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.10782	0.263372	ENSG00000243402.1
rs3180	Whole blood_ENSG00000166	6 0.912352	2.198	0.545525	3.636475	NUDT13	Whole blo	GTEEx_v6	G	A	73883196	10 rs1245578	-0.04089	0.266781	ENSG00000166321.9
rs3180	Pituitary_ENSG00000272627.	20 0.351072	-3.639	0.547246	6.04541	RP11-354	Pituitary	GTEEx_v6	T	C	73762673	10 rs2219837	0.124079	0.261343	ENSG00000272627.1
rs3180	Brain caudate basal ganglia_E	1 NA	-3.452	0.54737	5.737062	DNAJC9-A	Brain caud	GTEEx_v6	C	G	74046191	10 rs1074039	-0.05765	0.265596	ENSG00000236756.4
rs3180	Colon transverse_ENSG00000	20 0.125426	-1.105	0.548114	1.839332	DNAJB12	Colon tran	GTEEx_v6	T	C	73762673	10 rs2219837	0.03767	0.261496	ENSG00000148719.10
rs3180	Breast mammary tissue_ENSG	20 0.491319	-1.413	0.548688	2.355858	MICU1	Breast mai	GTEEx_v6	T	C	73762673	10 rs2219837	0.048179	0.261117	ENSG00000107745.12
rs7814941	Cells EBV-transformed lympho	19 0.77507	-1.382	0.548961	2.305912	FAM49B	Cells EBV-t	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.06136	0.260227	ENSG00000153310.14
rs7814941	Brain anterior cingulate corre	16 0.328758	3.093	0.549049	5.16282	RP11-473C	Brain ante	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.137351	0.259182	ENSG00000253720.1
rs3180	Brain cerebellar hemisphere_	20 0.419883	2.791	0.549301	4.660834	RP11-150C	Brain cere	GTEEx_v6	T	C	73762673	10 rs2219837	-0.09517	0.259761	ENSG00000272988.1
rs3180	Heart left ventricle_ENSG000	20 0.387757	-1.918	0.549367	3.203137	Y_RNA	Heart left \t	GTEEx_v6	T	C	73762673	10 rs2219837	0.065395	0.260608	ENSG00000200170.1
rs7814941	Testis_ENSG00000153317.10	19 0.663229	0.966	0.55002	1.616591	ASAP1	Testis	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.042903	0.259667	ENSG00000153317.10
rs7814941	Colon transverse_ENSG00000	19 0.268277	1.419	0.551003	2.380204	RP11-473C	Colon tran	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.063013	0.258963	ENSG00000254317.1
rs3180	Breast mammary tissue_ENSG	20 0.606642	1.182	0.551715	1.986134	CHST3	Breast mai	GTEEx_v6	T	C	73762673	10 rs2219837	-0.04031	0.258709	ENSG00000122863.5
rs3180	Muscle skeletal_ENSG000002	20 0.64492	1.098	0.552625	1.849423	UNC5B-AS	Muscle ske	GTEEx_v6	T	C	73762673	10 rs2219837	-0.03745	0.25838	ENSG00000237512.2
rs3180	Skin sun exposed lower leg_EI	20 0.53205	0.579	0.552954	0.976232	PSAP	Skin sun ei	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01975	0.258044	ENSG00000197746.9
rs3180	Spleen_ENSG00000168209.4	20 0.07207	2.330	0.554035	3.936896	DDIT4	Spleen	GTEEx_v6	T	C	73762673	10 rs2219837	-0.07944	0.256024	ENSG00000168209.4
rs7814941	Brain hippocampus_ENSG000	17 0.065169	-2.012	0.554767	3.406247	RP11-473C	Brain hipp	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.08933	0.255013	ENSG00000254317.1
rs3180	Skin not sun exposed suprapu	20 0.20839	1.174	0.555212	1.990056	C10orf54	Skin not su	GTEEx_v6	T	C	73762673	10 rs2219837	-0.04004	0.256001	ENSG00000107738.15
rs3180	Uterus_ENSG00000214688.4	20 0.908216	2.681	0.555232	4.545011	C10orf105	Uterus	GTEEx_v6	T	C	73762673	10 rs2219837	-0.09143	0.254514	ENSG00000214688.4
rs3180	Brain putamen basal ganglia_	20 0.148166	-1.723	0.555574	2.92337	ASCC1	Brain puta	GTEEx_v6	T	C	73762673	10 rs2219837	0.058758	0.254635	ENSG00000138303.13
rs3180	Brain cerebellar hemisphere_	20 0.417684	-1.595	0.555713	2.707764	ANAPC16	Brain cere	GTEEx_v6	T	C	73762673	10 rs2219837	0.054406	0.254707	ENSG00000166295.4
rs3180	Thyroid_ENSG00000166295.4	20 0.070496	0.599	0.55578	1.016102	ANAPC16	Thyroid	GTEEx_v6	T	C	73762673	10 rs2219837	-0.02041	0.255766	ENSG00000166295.4
rs7814941	Adipose subcutaneous_ENSG	20 0.313856	-0.504	0.55585	0.85631	ASAP1	Adipose su	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.02239	0.255521	ENSG00000153317.10
rs3180	Cells transformed fibroblasts_	20 0.749933	-0.830	0.556111	1.41038	MCU	Cells trans	GTEEx_v6	T	C	73762673	10 rs2219837	0.028309	0.255495	ENSG00000156026.10
rs3180	Brain anterior cingulate corre	8 0.823456	2.730	0.556972	4.648858	P4HA1	Brain ante	GTEEx_v6	T	C	73858549	10 rs1668156	-0.05106	0.255629	ENSG00000122884.8
rs3180	Vagina_ENSG00000227382.1	1 NA	-6.973	0.557207	11.87902	EIF4A2P2	Vagina	GTEEx_v6	C	G	74046191	10 rs1074039	-0.11645	0.25703	ENSG00000227382.1
rs3180	Nerve tibial_ENSG000001228	8 0.040992	-1.823	0.557814	3.110232	P4HA1	Nerve tibi	GTEEx_v6	T	C	73858549	10 rs1668156	0.034088	0.256558	ENSG00000122884.8
rs7814941	Pituitary_ENSG00000254317.	18 0.260056	-1.967	0.558241	3.360157	RP11-473C	Pituitary	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.08734	0.252465	ENSG00000254317.1
rs3180	Ovary_ENSG00000227540.1	1 NA	2.984	0.559298	5.110875	RP11-152	Ovary	GTEEx_v6	C	G	74046191	10 rs1074039	0.049836	0.255504	ENSG00000227540.1

rs3180	Adrenal gland_ENSG00000122884.8	8	0.994803	-3.606	0.559441	6.177748	P4HA1	Adrenal gl ^c GTEx_v6	T	C	73858549	10	rs1668156	0.067428	0.254733	ENSG00000122884.8
rs12310519	Uterus_ENSG00000134532.11	11	0.806448	-1.858	0.560408	3.190816	SOX5	Uterus GTEx_v6	C	T	23982559	12	rs9804988	0.107567	0.250179	ENSG00000134532.11
rs3180	Artery aorta_ENSG0000018210	1	NA	-1.458	0.560705	2.506499	MRPS16	Artery aor ^c GTEx_v6	C	G	74046191	10	rs1074039	-0.02435	0.25534	ENSG0000018210.9
rs12310519	Artery coronary_ENSG000001	11	0.476843	-1.288	0.561635	2.218422	SOX5	Artery cor ^c GTEx_v6	C	T	23982559	12	rs9804988	0.074552	0.25024	ENSG00000134532.11
rs3180	Colon sigmoid_ENSG00000107736.15	20	0.287916	-2.175	0.561982	3.751287	CDH23	Colon sign ^r GTEx_v6	T	C	73762673	10	rs2219837	0.07418	0.250341	ENSG00000107736.15
rs3180	Lung_ENSG00000107738.15	20	0.654911	0.877	0.562073	1.512907	C10orf54	Lung GTEx_v6	T	C	73762673	10	rs2219837	-0.02991	0.250832	ENSG00000107738.15
rs3180	Muscle skeletal_ENSG00000230526.1	20	0.231364	1.252	0.562582	2.162872	RP11-472C	Muscle ske ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.0427	0.250547	ENSG000000230526.1
rs7814941	Brain cortex_ENSG0000015331.10	18	0.890065	1.464	0.562587	2.528481	ASAP1	Brain cort ^e GTEx_v6	A	G	1.31E+08	8	rs1095648	0.065002	0.249285	ENSG0000015331.10
rs3180	Colon sigmoid_ENSG00000236756.4	1	NA	-4.185	0.563367	7.241717	DNAJC9-A ^c	Colon sign ^r GTEx_v6	C	G	74046191	10	rs1074039	-0.06988	0.252817	ENSG000000236756.4
rs3180	Muscle skeletal_ENSG00000166295.4	20	0.082062	0.566	0.563401	0.979482	ANAPC16	Muscle ske ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.0193	0.249909	ENSG000000166295.4
rs3180	Brain cerebellar hemisphere_	20	0.110901	-2.227	0.564504	3.864911	CDH23	Brain cere ^r GTEx_v6	T	C	73762673	10	rs2219837	0.075935	0.247872	ENSG00000107736.15
rs3180	Ovary_ENSG00000272599.1	5	0.250288	4.488	0.564691	7.793755	RP11-152N	Ovary GTEx_v6	C	T	73899093	10	rs1245515	-0.08348	0.249976	ENSG000000272599.1
rs3180	Uterus_ENSG00000107745.12	20	0.199709	-2.568	0.564732	4.459839	MICU1	Uterus GTEx_v6	T	C	73762673	10	rs2219837	0.087572	0.247154	ENSG00000107745.12
rs3180	Liver_ENSG00000138303.13	20	0.212783	-2.026	0.566008	3.530532	ASCC1	Liver GTEx_v6	T	C	73762673	10	rs2219837	0.069097	0.246872	ENSG000000138303.13
rs3180	Colon sigmoid_ENSG00000166321.9	6	0.457638	-2.817	0.566359	4.912434	NUDT13	Colon sign ^r GTEx_v6	G	A	73883196	10	rs1245578	0.052394	0.249242	ENSG000000166321.9
rs3180	Brain caudate basal ganglia_E	1	NA	2.970	0.567845	5.198478	MRPS16	Brain caud GTEx_v6	C	G	74046191	10	rs1074039	0.049591	0.248921	ENSG00000182180.9
rs12310519	Brain anterior cingulate cortex	11	0.728952	2.481	0.568075	4.345077	RP11-444C	Brain ante ^r GTEx_v6	C	T	23982559	12	rs9804988	-0.14362	0.244342	ENSG000000255864.1
rs3180	Adipose visceral omentum_E	20	0.539939	1.840	0.568315	3.224491	NPM1P24	Adipose vi ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.06273	0.245746	ENSG000000215086.2
rs3180	Skin not sun exposed suprapu	20	0.892928	2.013	0.568528	3.529934	RP11-354E	Skin not su ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.06864	0.245627	ENSG000000272627.1
rs3180	Cells transformed fibroblasts_	20	0.305624	0.830	0.569015	1.457649	SLC29A3	Cells trans ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.02831	0.245442	ENSG000000198246.7
rs7814941	Brain cortex_ENSG00000253720.1	18	0.744452	2.094	0.569115	3.67842	RP11-473C	Brain cort ^e GTEx_v6	A	G	1.31E+08	8	rs1095648	0.092988	0.244271	ENSG000000253720.1
rs3180	Breast mammary tissue_ENSG	20	0.487491	-1.458	0.570295	2.568137	DDIT4	Breast mai ^r GTEx_v6	T	C	73762673	10	rs2219837	0.049708	0.244214	ENSG000000168209.4
rs3180	Colon transverse_ENSG000000	1	NA	3.459	0.570348	6.094072	DNAJC9-A ^c	Colon tran ^r GTEx_v6	C	G	74046191	10	rs1074039	0.057759	0.24745	ENSG000000236756.4
rs3180	Adipose visceral omentum_E	20	0.241412	-1.111	0.570493	1.958769	SLC29A3	Adipose vi ^r GTEx_v6	T	C	73762673	10	rs2219837	0.037894	0.244073	ENSG000000198246.7
rs12310519	Heart atrial appendage_ENSG	11	0.194446	-1.416	0.570769	2.498137	RP11-444C	Heart atria ^r GTEx_v6	C	T	23982559	12	rs9804988	0.082	0.243436	ENSG000000255864.1
rs3180	Brain cortex_ENSG00000272630.1	8	0.353965	-3.481	0.570909	6.141899	RP11-344N	Brain cort ^e GTEx_v6	T	C	73865131	10	rs1100017	0.064741	0.245293	ENSG000000272630.1
rs12310519	Brain hypothalamus_ENSG000000	11	0.071711	-2.549	0.571567	4.505716	RP11-444C	Brain hypc ^r GTEx_v6	C	T	23982559	12	rs9804988	0.147592	0.241986	ENSG000000255864.1
rs3180	Brain caudate basal ganglia_E	8	0.497371	4.052	0.573349	7.195145	RP11-344N	Brain caud GTEx_v6	T	C	73865131	10	rs1100017	-0.07536	0.243458	ENSG000000272630.1
rs3180	Whole blood_ENSG000001380.8	20	0.06325	-1.141	0.573452	2.027569	PLA2G12B	Whole blo ^r GTEx_v6	T	C	73762673	10	rs2219837	0.038924	0.242133	ENSG00000013830.8
rs3180	Ovary_ENSG00000122884.8	8	0.192926	-2.289	0.574556	4.077735	P4HA1	Ovary GTEx_v6	T	C	73858549	10	rs1668156	0.042805	0.242215	ENSG000000122884.8
rs3180	Adipose subcutaneous_ENSG	1	NA	2.028	0.575223	3.619863	DNAJC9	Adipose su ^r GTEx_v6	C	G	74046191	10	rs1074039	0.033876	0.243944	ENSG000000213551.4
rs3180	Colon sigmoid_ENSG00000215086.2	20	0.756264	-2.365	0.575609	4.223982	NPM1P24	Colon sign ^r GTEx_v6	T	C	73762673	10	rs2219837	0.080634	0.239879	ENSG000000215086.2
rs3180	Muscle skeletal_ENSG00000227382.1	1	NA	2.778	0.576591	4.975973	EIF4A2P2	Muscle ske ^r GTEx_v6	C	G	74046191	10	rs1074039	0.0464	0.242938	ENSG000000227382.1
rs3180	Heart left ventricle_ENSG000000	1	NA	-1.483	0.576748	2.656528	MRPS16	Heart left ^r GTEx_v6	C	G	74046191	10	rs1074039	-0.02476	0.242487	ENSG000000182180.9
rs3180	Esophagus muscularis_ENSG00	20	0.612878	-1.089	0.576885	1.951434	DDIT4	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	0.037128	0.239316	ENSG000000168209.4
rs3180	Skin not sun exposed suprapu	8	0.214205	2.592	0.577354	4.651798	RP11-344N	Skin not su ^r GTEx_v6	T	C	73865131	10	rs1100017	-0.04822	0.240971	ENSG000000272630.1
rs3180	Whole blood_ENSG000000197746.9	20	0.713916	0.622	0.577751	1.116684	PSAP	Whole blo ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.0212	0.238862	ENSG000000197746.9
rs12310519	Colon transverse_ENSG000000	11	0.844266	1.112	0.578141	1.999741	RP11-444C	Colon tran ^r GTEx_v6	C	T	23982559	12	rs9804988	-0.06439	0.237905	ENSG000000255864.1
rs3180	Brain cortex_ENSG0000001077	20	0.646672	-1.924	0.578442	3.461992	CDH23	Brain cort ^e GTEx_v6	T	C	73762673	10	rs2219837	0.065598	0.237391	ENSG000000107736.15
rs3180	Pituitary_ENSG00000122882.1	1	NA	-2.792	0.580072	5.046646	ECD	Pituitary GTEx_v6	C	G	74046191	10	rs1074039	-0.04663	0.239046	ENSG000000122882.6
rs3180	Heart left ventricle_ENSG000000	16	0.777479	0.900	0.580263	1.627985	RPL17P50	Heart left ^r GTEx_v6	A	G	73820622	10	rs3180	-0.02998	0.236672	ENSG000000213700.3
rs7814941	Skin sun exposed lower leg_EI	20	0.843633	0.924	0.580527	1.671231	RP11-473C	Skin sun e ^r GTEx_v6	A	G	1.31E+08	8	rs1095648	0.041006	0.236537	ENSG000000254317.1
rs3180	Nerve tibial_ENSG00000166228.4	2	NA	1.405	0.581602	2.550075	PCBD1	Nerve tibi ^r GTEx_v6	C	T	73646408	10	rs1437267	0.030774	0.238325	ENSG000000166228.4
rs3180	Lung_ENSG00000122884.8	8	0.077278	1.352	0.582259	2.45766	P4HA1	Lung GTEx_v6	T	C	73858549	10	rs1668156	-0.02528	0.237342	ENSG000000122884.8
rs7814941	Artery tibial_ENSG0000015331.10	20	0.245662	-0.617	0.583424	1.125378	FAM49B	Artery tibi ^r GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.0274	0.234337	ENSG000000153310.14
rs3180	Esophagus gastroesophageal	20	0.778559	1.245	0.583493	2.270071	ANAPC16	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	-0.04244	0.233968	ENSG000000166295.4
rs3180	Adipose subcutaneous_ENSG	20	0.291148	-0.552	0.584186	1.00819	MCU	Adipose su ^r GTEx_v6	T	C	73762673	10	rs2219837	0.018815	0.233961	ENSG000000156026.10
rs3180	Nerve tibial_ENSG0000019774.9	20	0.067697	-0.570	0.584445	1.041406	PSAP	Nerve tibi ^r GTEx_v6	T	C	73762673	10	rs2219837	0.019422	0.233698	ENSG000000197746.9
rs3180	Skin sun exposed lower leg_EI	8	0.72095	-0.989	0.585415	1.812216	P4HA1	Skin sun e ^r GTEx_v6	T	C	73858549	10	rs1668156	0.018486	0.234955	ENSG000000122884.8
rs3180	Brain cerebellar hemisphere_	20	0.097157	2.048	0.585838	3.758841	OIT3	Brain cere ^r GTEx_v6	T	C	73762673	10	rs2219837	-0.06984	0.231732	ENSG000000138315.8

rs7814941	Brain caudate basal ganglia_E	18	0.326943	1.704	0.586658	3.13413	GSDMC	Brain caud GTE _{v6}	A	G	1.31E+08	8	rs1095648	0.075657	0.23114	ENSG00000147697.4
rs3180	Muscle skeletal_ENSG000001	1	NA	1.541	0.587532	2.841069	ECD	Muscle ske GTE _{v6}	C	G	74046191	10	rs1074039	0.025735	0.234405	ENSG00000122882.6
rs3180	Artery aorta_ENSG000001228	8	0.784773	1.404	0.587536	2.587787	P4HA1	Artery aort GTE _{v6}	T	C	73858549	10	rs1668156	-0.02625	0.233119	ENSG00000122884.8
rs3180	Esophagus mucosa_ENSG0000	8	0.267248	1.715	0.588285	3.168393	P4HA1	Esophagus GTE _{v6}	T	C	73858549	10	rs1668156	-0.03207	0.232671	ENSG00000122884.8
rs3180	Brain cerebellum_ENSG0000	5	0.062764	4.669	0.589156	8.645669	RP11-152A1	Brain cere GTE _{v6}	C	T	73899093	10	rs1245515	-0.08685	0.231369	ENSG00000272599.1
rs7814941	Pituitary_ENSG00000153310.	18	0.936329	1.434	0.589762	2.660232	FAM49B	Pituitary GTE _{v6}	A	G	1.31E+08	8	rs1095648	0.063685	0.228623	ENSG00000153310.14
rs3180	Thyroid_ENSG00000272627.1	20	0.559884	1.359	0.590475	2.525298	RP11-354E	Thyroid GTE _{v6}	T	C	73762673	10	rs2219837	-0.04634	0.229244	ENSG00000272627.1
rs3180	Spleen_ENSG00000166321.9	6	0.369561	-3.632	0.592979	6.79512	NUDT13	Spleen GTE _{v6}	G	A	73883196	10	rs1245578	0.067558	0.228263	ENSG00000166321.9
rs7814941	Uterus_ENSG00000153317.1C	16	0.493775	-1.879	0.593025	3.515244	ASAP1	Uterus GTE _{v6}	A	G	1.31E+08	8	rs1095648	-0.08342	0.225792	ENSG00000153317.10
rs3180	Thyroid_ENSG00000213700.3	16	0.677526	0.611	0.593455	1.144011	RPL17P50	Thyroid GTE _{v6}	A	G	73820622	10	rs3180	-0.02034	0.227048	ENSG00000213700.3
rs7814941	Heart left ventricle_ENSG0000	19	0.552982	0.547	0.593973	1.025844	FAM49B	Heart left GTE _{v6}	A	G	1.31E+08	8	rs1095648	0.024281	0.2263	ENSG00000153310.14
rs3180	Brain caudate basal ganglia_E	20	0.427783	-1.723	0.594034	3.231956	DDIT4	Brain caud GTE _{v6}	T	C	73762673	10	rs2219837	0.058742	0.225871	ENSG00000168209.4
rs3180	Prostate_ENSG00000182180.!	1	NA	-2.326	0.595141	4.376338	MRPS16	Prostate GTE _{v6}	C	G	74046191	10	rs1074039	-0.03884	0.227524	ENSG00000182180.9
rs3180	Brain hippocampus_ENSG0000	1	NA	-5.138	0.59528	9.67203	RP11-152A1	Brain hippoc GTE _{v6}	C	G	74046191	10	rs1074039	-0.0858	0.227262	ENSG00000227540.1
rs3180	Brain caudate basal ganglia_E	20	0.682889	3.061	0.596812	5.786654	RP11-354E	Brain caud GTE _{v6}	T	C	73762673	10	rs2219837	-0.10438	0.223384	ENSG00000272627.1
rs3180	Adipose visceral omentum_E	20	0.288031	1.629	0.597563	3.085518	RP11-354E	Adipose vis <i>o</i> GTE _{v6}	T	C	73762673	10	rs2219837	-0.05554	0.223809	ENSG00000272627.1
rs12310519	Brain cerebellar hemisphere_	11	0.453101	-0.979	0.597698	1.855577	SOX5	Brain cere GTE _{v6}	C	T	23982559	12	rs9804988	0.056696	0.222791	ENSG00000134532.11
rs3180	Thyroid_ENSG00000138308.5	20	0.893129	1.377	0.599271	2.621054	PLA2G12B	Thyroid GTE _{v6}	T	C	73762673	10	rs2219837	-0.04696	0.222776	ENSG00000138308.5
rs3180	Pituitary_ENSG00000138303.:	20	0.026558	2.648	0.599419	5.0418	ASCC1	Pituitary GTE _{v6}	T	C	73762673	10	rs2219837	-0.0903	0.221726	ENSG00000138303.13
rs3180	Brain putamen basal ganglia_	1	NA	-3.345	0.599769	6.374974	MRPS16	Brain puta GTE _{v6}	C	G	74046191	10	rs1074039	-0.05586	0.223917	ENSG00000182180.9
rs7814941	Whole blood_ENSG00000254:	20	0.070479	0.474	0.599844	0.904353	RP11-473C	Whole blo GTE _{v6}	A	G	1.31E+08	8	rs1095648	0.021065	0.222278	ENSG00000254317.1
rs7814941	Heart atrial appendage_ENSG	19	0.55192	-1.297	0.600815	2.478797	RP11-473C	Heart atria GTE _{v6}	A	G	1.31E+08	8	rs1095648	-0.05759	0.221167	ENSG00000254317.1
rs3180	Brain nucleus accumbens basa	20	0.550189	1.546	0.60167	2.960804	CHST3	Brain nucle GTE _{v6}	T	C	73762673	10	rs2219837	-0.0527	0.220207	ENSG00000122863.5
rs3180	Esophagus mucosa_ENSG0000	20	0.328613	-1.032	0.602307	1.98081	C10orf54	Esophagus GTE _{v6}	T	C	73762673	10	rs2219837	0.035197	0.22051	ENSG00000107738.15
rs3180	Heart atrial appendage_ENSG	20	0.337787	-1.577	0.602931	3.031237	OIT3	Heart atria GTE _{v6}	T	C	73762673	10	rs2219837	0.05377	0.219782	ENSG00000138315.8
rs7814941	Esophagus gastroesophageal	19	0.435009	0.993	0.603692	1.913632	FAM49B	Esophagus GTE _{v6}	A	G	1.31E+08	8	rs1095648	0.044105	0.218977	ENSG00000153310.14
rs3180	Brain cerebellar hemisphere_	1	NA	-3.448	0.603824	6.643967	DNAJC9	Brain cereb GTE _{v6}	C	G	74046191	10	rs1074039	-0.05758	0.22104	ENSG00000213551.4
rs3180	Esophagus gastroesophageal	20	0.754998	1.300	0.604393	2.509565	MCU	Esophagus GTE _{v6}	T	C	73762673	10	rs2219837	-0.04434	0.218618	ENSG00000156026.10
rs3180	Brain cerebellum_ENSG00000	8	0.516283	2.305	0.605036	4.456571	P4HA1	Brain cereb GTE _{v6}	T	C	73858549	10	rs1668156	-0.0431	0.219509	ENSG00000122884.8
rs7814941	Breast mammary tissue_ENSG	20	0.977519	0.571	0.606646	1.109284	FAM49B	Breast mai GTE _{v6}	A	G	1.31E+08	8	rs1095648	0.025358	0.21707	ENSG00000153310.14
rs3180	Artery aorta_ENSG000001663	6	0.110623	-2.363	0.606743	4.591456	NUDT13	Artery aort GTE _{v6}	G	A	73883196	10	rs1245578	0.043958	0.218785	ENSG00000166321.9
rs3180	Skin not sun exposed suprapu	1	NA	-1.848	0.60706	3.592633	DNAJC9	Skin not su GTE _{v6}	C	G	74046191	10	rs1074039	-0.03085	0.219357	ENSG00000213551.4
rs3180	Heart left ventricle_ENSG0000	8	0.625642	2.778	0.607771	5.412338	RP11-344A1	Heart left GTE _{v6}	T	C	73865131	10	rs1100017	-0.05167	0.218006	ENSG00000272630.1
rs3180	Prostate_ENSG00000166295.	20	0.521058	1.275	0.608087	2.486367	ANAPC16	Prostate GTE _{v6}	T	C	73762673	10	rs2219837	-0.04348	0.215506	ENSG00000166295.4
rs3180	Ovary_ENSG00000213551.4	1	NA	-4.503	0.608091	8.781604	DNAJC9	Ovary GTE _{v6}	C	G	74046191	10	rs1074039	-0.0752	0.217826	ENSG00000213551.4
rs3180	Thyroid_ENSG00000168209.4	20	0.849219	-0.969	0.608667	1.892171	DDIT4	Thyroid GTE _{v6}	T	C	73762673	10	rs2219837	0.033034	0.215972	ENSG00000168209.4
rs3180	Artery coronary_ENSG000001	20	0.804826	-1.144	0.608673	2.234098	PSAP	Artery cor GTE _{v6}	T	C	73762673	10	rs2219837	0.039003	0.21547	ENSG00000197746.9
rs3180	Cells EBV-transformed lympho	1	NA	-3.206	0.609394	6.275419	RP11-152A1	Cells EBV-t GTE _{v6}	C	G	74046191	10	rs1074039	-0.05355	0.217254	ENSG00000227540.1
rs12310519	Ovary_ENSG00000134532.11	11	0.488224	-1.577	0.610415	3.0951	SOX5	Ovary GTE _{v6}	T	C	23982559	12	rs9804988	0.091302	0.213609	ENSG00000134532.11
rs3180	Lung_ENSG00000107731.8	20	0.130726	0.992	0.610904	1.94891	UNC5B	Lung GTE _{v6}	T	C	73762673	10	rs2219837	-0.03381	0.214368	ENSG00000107731.8
rs7814941	Breast mammary tissue_ENSG	20	0.611973	-0.840	0.611873	1.654746	GSDMC	Breast mai GTE _{v6}	A	G	1.31E+08	8	rs1095648	-0.03728	0.213332	ENSG00000147697.4
rs3180	Skin sun exposed lower leg_EI	5	0.93518	-2.374	0.612082	4.68224	SNORA11	Skin sun e GTE _{v6}	C	T	73899093	10	rs1245515	0.044164	0.215073	ENSG00000221164.1
rs3180	Brain hippocampus_ENSG0000	6	0.440978	-3.217	0.61304	6.360642	NUDT13	Brain hippoc GTE _{v6}	G	A	73883196	10	rs1245578	0.059833	0.213332	ENSG00000166321.9
rs3180	Brain nucleus accumbens basa	1	NA	-2.588	0.613989	5.131848	FAM149B1	Brain nucle GTE _{v6}	C	G	74046191	10	rs1074039	-0.04323	0.213627	ENSG00000138286.10
rs3180	Brain nucleus accumbens basa	2	NA	2.033	0.614447	4.035252	PCBD1	Brain nucle GTE _{v6}	C	T	73646408	10	rs1437267	0.044516	0.2129	ENSG00000166228.4
rs3180	Prostate_ENSG00000272630.:	8	0.509011	4.056	0.614455	8.052575	RP11-344A1	Prostate GTE _{v6}	T	C	73865131	10	rs1100017	-0.07545	0.212453	ENSG00000272630.1
rs3180	Esophagus gastroesophageal	20	0.31395	-1.245	0.615712	2.481322	MICU1	Esophagus GTE _{v6}	T	C	73762673	10	rs2219837	0.04247	0.210529	ENSG00000107745.12
rs3180	Spleen_ENSG00000166295.4	20	0.832047	1.305	0.616553	2.605622	ANAPC16	Spleen GTE _{v6}	T	C	73762673	10	rs2219837	-0.04449	0.209516	ENSG00000166295.4
rs12310519	Pituitary_ENSG00000256321.:	11	0.250897	1.632	0.617575	3.268326	RP11-153K	Pituitary GTE _{v6}	C	T	23982559	12	rs9804988	-0.09448	0.208575	ENSG00000256321.1
rs3180	Brain frontal cortex BA9_ENS	20	0.245099	1.234	0.617668	2.471357	C10orf54	Brain front GTE _{v6}	T	C	73762673	10	rs2219837	-0.04207	0.20878	ENSG00000107738.15

rs3180	Thyroid_ENSG00000107738.1	20	0.040946	-0.760	0.619032	1.529434	C10orf54	Thyroid	GTEEx_v6	T	C	73762673	10	rs2219837	0.025932	0.208591	ENSG00000107738.15
rs3180	Adipose visceral omentum_E	20	0.513403	0.999	0.620831	2.020081	CDH23	Adipose vi	GTEEx_v6	T	C	73762673	10	rs2219837	-0.03408	0.207131	ENSG00000107736.15
rs3180	Muscle skeletal_ENSG0000021	20	0.659842	1.074	0.622219	2.180481	Y_RNA	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	-0.03664	0.206431	ENSG00000200170.1
rs7814941	Brain nucleus accumbens bas	18	0.893511	-0.509	0.622752	1.034818	FAM49B	Brain nucle	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.0226	0.20511	ENSG00000153310.14
rs3180	Nerve tibial_ENSG000002725	5	0.338022	2.014	0.623045	4.09766	RP11-152	Nerve tibi	GTEEx_v6	C	T	73899093	10	rs1245515	-0.03746	0.2071	ENSG00000272599.1
rs3180	Brain hippocampus_ENSG000	20	0.306749	-0.953	0.62317	1.938892	ANAPC16	Brain hippoc	GTEEx_v6	T	C	73762673	10	rs2219837	0.032487	0.204726	ENSG00000166295.4
rs3180	Brain hypothalamus_ENSG00	5	0.401324	-5.008	0.623663	10.20624	RP11-152	Brain hypc	GTEEx_v6	C	T	73899093	10	rs1245515	0.093146	0.205732	ENSG00000272599.1
rs3180	Skin sun exposed lower leg_EI	8	0.280846	1.882	0.623754	3.836298	RP11-344	Skin sun e	GTEEx_v6	T	C	73865131	10	rs1100017	-0.035	0.206657	ENSG00000272630.1
rs3180	Whole blood_ENSG00000138	20	0.051753	0.645	0.624898	1.31931	ASCC1	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	-0.022	0.204535	ENSG00000138303.13
rs3180	Esophagus muscularis_ENSG0	1	NA	-3.141	0.625457	6.433811	EIF4A2P2	Esophagus	GTEEx_v6	C	G	74046191	10	rs1074039	-0.05245	0.205994	ENSG00000227382.1
rs3180	Esophagus muscularis_ENSG0	1	NA	1.863	0.62552	3.816599	FAM149B1	Esophagus	GTEEx_v6	C	G	74046191	10	rs1074039	0.031106	0.205949	ENSG00000138286.10
rs3180	Nerve tibial_ENSG000002135	1	NA	1.957	0.625833	4.013974	DNAJC9	Nerve tibi	GTEEx_v6	C	G	74046191	10	rs1074039	0.032686	0.205789	ENSG00000213551.4
rs3180	Brain anterior cingulate cort	20	0.246464	-1.159	0.626138	2.37955	MICU1	Brain ante	GTEEx_v6	T	C	73762673	10	rs2219837	0.03953	0.202439	ENSG00000107745.12
rs3180	Colon sigmoid_ENSG0000018	1	NA	-1.566	0.62657	3.218732	MRPS16	Colon sigmoid	GTEEx_v6	C	G	74046191	10	rs1074039	-0.02615	0.204877	ENSG00000182180.9
rs3180	Cells EBV-transformed lympho	20	0.395387	1.617	0.626759	3.325578	ASCC1	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05515	0.202681	ENSG00000138303.13
rs3180	Skin sun exposed lower leg_EI	20	0.386099	0.773	0.627353	1.591575	CHST3	Skin sun e	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02635	0.202786	ENSG00000122863.5
rs3180	Artery tibial_ENSG000001077	20	0.186578	0.711	0.630164	1.477267	C10orf54	Artery tibi	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02426	0.200814	ENSG00000107738.15
rs3180	Heart atrial appendage_ENSG	1	NA	-2.613	0.630298	5.429854	ECD	Heart atria	GTEEx_v6	C	G	74046191	10	rs1074039	-0.04364	0.202339	ENSG00000122882.6
rs3180	Lung_ENSG00000138315.8	20	0.237759	0.969	0.630521	2.01513	OIT3	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	-0.03305	0.200557	ENSG00000138315.8
rs7814941	Small intestine terminal ileum	16	0.546462	1.807	0.630707	3.758629	RP11-473C	Small intes	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.080226	0.199307	ENSG00000254317.1
rs3180	Brain anterior cingulate cort	20	0.748757	-1.132	0.632733	2.369026	ANAPC16	Brain ante	GTEEx_v6	T	C	73762673	10	rs2219837	0.038605	0.197899	ENSG00000166295.4
rs3180	Brain cortex_ENSG000001228	8	0.947101	2.179	0.632756	4.559535	P4HA1	Brain cortex	GTEEx_v6	T	C	73858549	10	rs1668156	-0.04074	0.199564	ENSG00000122884.8
rs3180	Brain cortex_ENSG000001662	20	0.788062	1.003	0.635164	2.113396	ANAPC16	Brain cort	GTEEx_v6	T	C	73762673	10	rs2219837	-0.03419	0.196695	ENSG00000166295.4
rs3180	Heart atrial appendage_ENSG	1	NA	2.849	0.635234	6.005194	RP11-152	Heart atria	GTEEx_v6	C	G	74046191	10	rs1074039	0.047573	0.198849	ENSG00000227540.1
rs3180	Muscle skeletal_ENSG000001	20	0.166584	0.717	0.636102	1.516115	C10orf54	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02446	0.196786	ENSG00000107738.15
rs3180	Cells EBV-transformed lympho	20	0.258058	-1.633	0.636944	3.460901	MICU1	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	0.055701	0.195666	ENSG00000107745.12
rs3180	Small intestine terminal ileum	20	0.087145	0.727	0.637446	1.542726	PLA2G12B	Small intes	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02479	0.194811	ENSG00000138308.5
rs3180	Brain anterior cingulate cort	20	0.369289	1.437	0.638383	3.05786	C10orf54	Brain ante	GTEEx_v6	T	C	73762673	10	rs2219837	-0.049	0.194048	ENSG00000107738.15
rs3180	Small intestine terminal ileum	20	0.219541	2.836	0.639063	6.046327	RP11-354E	Small intes	GTEEx_v6	T	C	73762673	10	rs2219837	-0.0967	0.193712	ENSG00000272627.1
rs3180	Brain anterior cingulate cort	20	0.679983	2.548	0.639373	5.438353	SLC29A3	Brain ante	GTEEx_v6	T	C	73762673	10	rs2219837	-0.0869	0.193378	ENSG00000198246.7
rs3180	Artery aorta_ENSG000002726	20	0.946827	1.523	0.639468	3.250305	RP11-354E	Artery aort	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05192	0.194265	ENSG00000272627.1
rs3180	Brain caudate basal ganglia_E	20	0.821494	-2.362	0.640091	5.051532	MCU	Brain caud	GTEEx_v6	T	C	73762673	10	rs2219837	0.080543	0.193386	ENSG00000156026.10
rs12310519	Nerve tibial_ENSG000001345	11	0.624568	-0.505	0.64051	1.081385	SOX5	Nerve tibi	GTEEx_v6	C	T	23982559	12	rs9804988	0.029239	0.193513	ENSG00000134532.11
rs3180	Artery coronary_ENSG000001	20	0.798105	1.025	0.640683	2.196474	CHST3	Artery cor	GTEEx_v6	T	C	73762673	10	rs2219837	-0.03496	0.193149	ENSG00000122863.5
rs3180	Stomach_ENSG00000236756	1	NA	-2.916	0.640966	6.252142	DNAJC9-A	Stomach	GTEEx_v6	C	G	74046191	10	rs1074039	-0.04869	0.194881	ENSG00000236756.4
rs3180	Brain putamen basal ganglia_	20	0.312242	-2.535	0.641418	5.442288	UNC5B-AS	Brain puta	GTEEx_v6	T	C	73762673	10	rs2219837	0.086429	0.192222	ENSG00000237512.2
rs3180	Brain cortex_ENSG000002375	20	0.879926	-1.768	0.641601	3.798653	UNC5B-AS	Brain cort	GTEEx_v6	T	C	73762673	10	rs2219837	0.060293	0.192314	ENSG00000237512.2
rs3180	Stomach_ENSG00000272630	8	0.792312	-2.362	0.643391	5.102386	RP11-34N	Stomach	GTEEx_v6	T	C	73865131	10	rs1100017	0.043937	0.192626	ENSG00000272630.1
rs7814941	Ovary_ENSG00000153310.14	17	0.691221	-1.241	0.643828	2.684192	FAM49B	Ovary	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.0551	0.190565	ENSG00000153310.14
rs3180	Colon sigmoid_ENSG0000019	20	0.274409	1.328	0.644527	2.878594	SLC29A3	Colon sigmoid	GTEEx_v6	T	C	73762673	10	rs2219837	-0.04529	0.190586	ENSG00000198246.7
rs3180	Artery aorta_ENSG000002150	20	0.196789	1.630	0.644668	3.53475	NPM1P24	Artery aor	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05559	0.190732	ENSG00000215086.2
rs3180	Adrenal gland_ENSG0000021	20	0.547406	1.725	0.645008	3.743755	C10orf105	Adrenal gl	GTEEx_v6	T	C	73762673	10	rs2219837	-0.05881	0.190275	ENSG00000214688.4
rs3180	Esophagus muscularis_ENSG0	1	NA	1.950	0.645053	4.233045	DNAJC9	Esophagus	GTEEx_v6	C	G	74046191	10	rs1074039	0.032564	0.192177	ENSG00000213551.4
rs3180	Esophagus muscularis_ENSG0	20	0.595387	0.832	0.645429	1.808106	MCU	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02837	0.190266	ENSG00000156026.10
rs3180	Thyroid_ENSG00000200356.1	1	NA	-2.248	0.645992	4.894422	RNU6-833	Thyroid	GTEEx_v6	C	G	74046191	10	rs1074039	-0.03754	0.191614	ENSG00000200356.1
rs3180	Heart left ventricle_ENSG000	1	NA	-1.805	0.646937	3.941941	ECD	Heart left \v	GTEEx_v6	C	G	74046191	10	rs1074039	-0.03015	0.190804	ENSG00000122882.6
rs3180	Muscle skeletal_ENSG000002	1	NA	-1.619	0.648579	3.552187	DNAJC9	Muscle ske	GTEEx_v6	C	G	74046191	10	rs1074039	-0.02704	0.189901	ENSG00000213551.4
rs3180	Testis_ENSG00000213700.3	16	0.842032	-1.079	0.650644	2.383582	RPL17P50	Testis	GTEEx_v6	A	G	73820622	10	rs3180	0.035946	0.186579	ENSG00000213700.3
rs3180	Adrenal gland_ENSG0000015	20	0.680821	-1.206	0.650951	2.66549	MCU	Adrenal gl	GTEEx_v6	T	C	73762673	10	rs2219837	0.041124	0.186282	ENSG00000156026.10
rs3180	Colon transverse_ENSG00000	20	0.115472	0.735	0.65156	1.626522	OIT3	Colon tran	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02505	0.186008	ENSG00000138315.8

rs3180	Adipose visceral omentum_E	8	0.536739	-0.948	0.688868	2.366451	P4HA1	Adipose vi: GTEEx_v6	T	C	73858549	10	rs1668156	0.017718	0.162488	ENSG00000122884.8
rs3180	Esophagus gastroesophageal j	20	0.834062	1.251	0.689079	3.12608	DDIT4	Esophagus GTEEx_v6	T	C	73762673	10	rs2219837	-0.04265	0.161526	ENSG00000168209.4
rs12310519	Stomach_ENSG00000255864.	11	0.884534	0.767	0.689299	1.918564	RP11-444C	Stomach GTEEx_v6	C	T	23982559	12	rs9804988	-0.04441	0.161405	ENSG00000255864.1
rs12310519	Testis_ENSG00000256852.1	11	0.466027	1.392	0.689416	3.482444	KNOP1P1	Testis GTEEx_v6	C	T	23982559	12	rs9804988	-0.08058	0.161291	ENSG00000256852.1
rs3180	Whole blood_ENSG000002726	8	0.459392	1.050	0.690525	2.637621	RP11-344N	Whole blo GTEEx_v6	T	C	73865131	10	rs1100017	-0.01953	0.161621	ENSG00000272630.1
rs3180	Brain frontal cortex BA9_ENS	20	0.41192	-1.686	0.691014	4.241352	UNC5B-AS	Brain front GTEEx_v6	T	C	73762673	10	rs2219837	0.057487	0.160053	ENSG00000237512.2
rs3180	Esophagus muscularis_ENSG0	20	0.524889	0.655	0.691506	1.649414	MICU1	Esophagus GTEEx_v6	T	C	73762673	10	rs2219837	-0.02232	0.16021	ENSG00000107745.12
rs3180	Skin not sun exposed suprapu	1	NA	1.546	0.691761	3.900379	FAM149B1	Skin not su GTEEx_v6	C	G	74046191	10	rs1074039	0.025824	0.161015	ENSG00000138286.10
rs3180	Colon transverse_ENSG00000	1	NA	1.511	0.691918	3.812229	DNAJC9	Colon tran GTEEx_v6	C	G	74046191	10	rs1074039	0.025227	0.160846	ENSG00000213551.4
rs7814941	Liver_ENSG00000254317.1	17	0.585975	1.435	0.693189	3.638296	RP11-473C	Liver GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.063733	0.158681	ENSG00000254317.1
rs3180	Artery aorta_ENSG000002726	8	0.317933	1.644	0.694441	4.184731	RP11-344N	Artery aor GTEEx_v6	T	C	73865131	10	rs1100017	-0.03058	0.158975	ENSG00000272630.1
rs3180	Lung_ENSG00000138308.5	20	0.028431	0.591	0.694487	1.504269	PLA2G12B	Lung GTEEx_v6	T	C	73762673	10	rs2219837	-0.02015	0.158403	ENSG00000138308.5
rs7814941	Whole blood_ENSG00000254	20	0.902492	-0.628	0.694616	1.599298	RP11-473C	Whole blo GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.02788	0.158309	ENSG00000254263.1
rs3180	Artery tibial_ENSG000001982	20	0.717841	-0.559	0.695119	1.426948	SLC29A3	Artery tibi: GTEEx_v6	T	C	73762673	10	rs2219837	0.01907	0.158013	ENSG00000198246.7
rs3180	Artery aorta_ENSG000002275	1	NA	-1.713	0.698002	4.414737	RP11-152N	Artery aor: GTEEx_v6	C	G	74046191	10	rs1074039	-0.02861	0.157038	ENSG00000227540.1
rs3180	Brain cerebellum_ENSG00000	1	NA	-1.873	0.698395	4.833778	MRPS16	Brain cere: GTEEx_v6	C	G	74046191	10	rs1074039	-0.03128	0.156474	ENSG00000182180.9
rs3180	Pituitary_ENSG00000166321.1	6	0.036155	-2.809	0.698839	7.259986	NUDT13	Pituitary GTEEx_v6	G	A	73883196	10	rs1245578	0.052244	0.155726	ENSG00000166321.9
rs3180	Esophagus mucosa_ENSG00000	20	0.924345	-0.760	0.698863	1.965461	DDIT4	Esophagus GTEEx_v6	T	C	73762673	10	rs2219837	0.025928	0.155632	ENSG00000168209.4
rs3180	Esophagus muscularis_ENSG0	8	0.750516	1.041	0.698949	2.690563	P4HA1	Esophagus GTEEx_v6	T	C	73858549	10	rs1668156	-0.01946	0.156153	ENSG00000122884.8
rs12310519	Uterus_ENSG00000255864.1	11	0.895731	1.323	0.699143	3.423013	RP11-444C	Uterus GTEEx_v6	C	T	23982559	12	rs9804988	-0.0766	0.154589	ENSG00000255864.1
rs3180	Esophagus mucosa_ENSG00000	2	NA	-1.259	0.699201	3.25865	PCBD1	Esophagus GTEEx_v6	C	T	73646408	10	rs1437267	-0.02758	0.156185	ENSG00000166228.4
rs3180	Uterus_ENSG00000166321.9	6	0.062024	3.214	0.701682	8.389748	NUDT13	Uterus GTEEx_v6	G	A	73883196	10	rs1245578	-0.05977	0.153693	ENSG00000166321.9
rs3180	Lung_ENSG00000227382.1	1	NA	-1.980	0.701691	5.170184	EIF4A2P2	Lung GTEEx_v6	C	G	74046191	10	rs1074039	-0.03307	0.154807	ENSG00000227382.1
rs12310519	Adrenal gland_ENSG00000134	11	0.45619	0.937	0.701835	2.444822	SOX5	Adrenal gl: GTEEx_v6	C	T	23982559	12	rs9804988	-0.05427	0.15347	ENSG00000134532.11
rs3180	Artery coronary_ENSG000001	20	0.070682	-0.932	0.702748	2.442787	SPOCK2	Artery cor: GTEEx_v6	T	C	73762673	10	rs2219837	0.031788	0.152942	ENSG00000107742.8
rs7814941	Ovary_ENSG00000254317.1	17	0.876917	1.520	0.70394	3.999334	RP11-473C	Ovary GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.067478	0.151895	ENSG00000254317.1
rs3180	Stomach_ENSG00000166295.	20	0.332853	-0.600	0.704318	1.580258	ANAPC16	Stomach GTEEx_v6	T	C	73762673	10	rs2219837	0.02045	0.152117	ENSG00000166295.4
rs3180	Brain cerebellar hemisphere_	20	0.649135	-1.369	0.705439	3.622033	C10orf105	Brain cere: GTEEx_v6	T	C	73762673	10	rs2219837	0.046686	0.151059	ENSG00000214688.4
rs3180	Heart atrial appendage_ENSG	20	0.689226	-1.293	0.705474	3.42203	NPM1P24	Heart atria GTEEx_v6	T	C	73762673	10	rs2219837	0.044103	0.151369	ENSG00000215086.2
rs3180	Heart atrial appendage_ENSG	8	0.232059	1.997	0.705823	5.291083	RP11-344N	Heart atria GTEEx_v6	T	C	73865131	10	rs1100017	-0.03715	0.151723	ENSG00000272630.1
rs3180	Stomach_ENSG00000148719.	20	0.286433	0.612	0.705924	1.621814	DNAJB12	Stomach GTEEx_v6	T	C	73762673	10	rs2219837	-0.02087	0.151125	ENSG00000148719.10
rs3180	Vagina_ENSG00000214688.4	20	0.113028	1.766	0.705974	4.679873	C10orf105	Vagina GTEEx_v6	T	C	73762673	10	rs2219837	-0.06021	0.150617	ENSG00000214688.4
rs3180	Heart atrial appendage_ENSG	20	0.729775	0.754	0.706985	2.005732	PLA2G12B	Heart atria GTEEx_v6	T	C	73762673	10	rs2219837	-0.02571	0.150439	ENSG00000138308.5
rs3180	Nerve tibial_ENSG000002726	20	0.334487	1.100	0.707006	2.925317	RP11-354E	Nerve tibi: GTEEx_v6	T	C	73762673	10	rs2219837	-0.0375	0.150598	ENSG00000272627.1
rs3180	Liver_ENSG00000107736.15	20	0.916412	1.205	0.708123	3.219912	CDH23	Liver GTEEx_v6	T	C	73762673	10	rs2219837	-0.04111	0.149491	ENSG00000107736.15
rs3180	Brain anterior cingulate corte	20	0.508708	1.802	0.708286	4.817378	MCU	Brain ante GTEEx_v6	T	C	73762673	10	rs2219837	-0.06146	0.149067	ENSG00000156026.10
rs3180	Whole blood_ENSG00000236	1	NA	1.659	0.708644	4.4339965	DNAJC9-A'	Whole blo GTEEx_v6	C	G	74046191	10	rs1074039	0.027707	0.150484	ENSG00000236756.4
rs3180	Skin not sun exposed suprapu	20	0.533982	0.802	0.709016	2.149956	DDIT4	Skin not su GTEEx_v6	T	C	73762673	10	rs2219837	-0.02736	0.149284	ENSG00000168209.4
rs3180	Brain cortex_ENSG000001487	20	0.723592	-1.088	0.710088	2.927855	DNAJB12	Brain cort GTEEx_v6	T	C	73762673	10	rs2219837	0.037114	0.148279	ENSG00000148719.10
rs3180	Colon sigmoid_ENSG0000019	20	0.635809	-0.881	0.710883	2.376185	PSAP	Colon sign GTEEx_v6	T	C	73762673	10	rs2219837	0.030035	0.147972	ENSG00000197746.9
rs3180	Colon sigmoid_ENSG0000015	20	0.918906	0.978	0.713598	2.664021	MCU	Colon sign GTEEx_v6	T	C	73762673	10	rs2219837	-0.0334	0.1463315	ENSG00000156026.10
rs3180	Testis_ENSG00000107742.8	20	0.758643	0.616	0.714285	1.681316	SPOCK2	Testis GTEEx_v6	T	C	73762673	10	rs2219837	-0.02099	0.145969	ENSG00000107742.8
rs3180	Liver_ENSG00000236756.4	1	NA	2.443	0.714339	6.673369	DNAJC9-A'	Liver GTEEx_v6	C	G	74046191	10	rs1074039	0.040793	0.146472	ENSG00000236756.4
rs3180	Brain nucleus accumbens basa	20	0.075046	1.339	0.714556	3.65972	DDIT4	Brain nucle GTEEx_v6	T	C	73762673	10	rs2219837	-0.04564	0.145531	ENSG00000168209.4
rs3180	Brain anterior cingulate corte	20	0.784319	-1.436	0.715906	3.946485	CDH23	Brain ante GTEEx_v6	T	C	73762673	10	rs2219837	0.048977	0.144438	ENSG00000107736.15
rs3180	Colon sigmoid_ENSG0000016	20	0.775374	-0.816	0.716334	2.244513	ANAPC16	Colon sign GTEEx_v6	T	C	73762673	10	rs2219837	0.027811	0.144653	ENSG00000166295.4
rs3180	Brain cerebellum_ENSG00000	6	0.463207	-2.456	0.716382	6.760909	NUDT13	Brain cerel GTEEx_v6	G	A	73883196	10	rs1245578	0.045686	0.145007	ENSG00000166321.9
rs3180	Ovary_ENSG00000200170.1	20	0.151487	1.858	0.71717	5.1293	Y_RNA	Ovary GTEEx_v6	T	C	73762673	10	rs2219837	-0.06336	0.143877	ENSG00000200170.1
rs3180	Adipose subcutaneous_ENSG0	16	0.795546	0.462	0.71726	1.276852	RPL17P50	Adipose su GTEEx_v6	A	G	73820622	10	rs3180	-0.0154	0.144366	ENSG00000213700.3
rs12310519	Artery aorta_ENSG000001345	11	0.470464	0.551	0.717383	1.523186	SOX5	Artery aor GTEEx_v6	C	T	23982559	12	rs9804988	-0.03192	0.144116	ENSG00000134532.11

rs3180	Lung_ENSG00000148719.10	20	0.100326	0.381	0.717447	1.052433	DNAJB12	Lung	GTEX_v6	T	C	73762673	10	rs2219837	-0.01299	0.144236	ENSG00000148719.10
rs3180	Spleen_ENSG00000272599.1	5	0.983854	2.852	0.717555	7.883618	RP11-152N	Spleen	GTEX_v6	C	T	73899093	10	rs1245515	-0.05304	0.14417	ENSG00000272599.1
rs7814941	Nerve_tibial_ENSG0000014769	20	0.434075	0.642	0.718039	1.778745	GSDMC	Nerve tibi	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.028517	0.143811	ENSG00000147697.4
rs3180	Brain_hypothalamus_ENSG000001	1	NA	-2.867	0.718256	7.947402	MRPS16	Brain hypc	GTEX_v6	C	G	74046191	10	rs1074039	-0.04788	0.143896	ENSG00000182180.9
rs3180	Thyroid_ENSG00000138315.8	20	0.269748	0.817	0.718441	2.266199	OIT3	Thyroid	GTEX_v6	T	C	73762673	10	rs2219837	-0.02786	0.143633	ENSG00000138315.8
rs7814941	Skin_not_sun_exposed_suprapu	20	0.67438	-0.663	0.718607	1.840134	ASAP1	Skin not su	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.02944	0.143393	ENSG00000153317.10
rs12310519	Testis_ENSG00000255745.1	11	0.713133	1.127	0.718892	3.131723	RP11-625L	Testis	GTEX_v6	C	T	23982559	12	rs904988	-0.06527	0.143112	ENSG00000255745.1
rs3180	Skin_not_sun_exposed_suprapu	5	0.045878	2.184	0.719489	6.081175	SNORA11	Skin not su	GTEX_v6	C	T	73899093	10	rs1245515	-0.04062	0.143389	ENSG00000221164.1
rs3180	Heart_atrial_appendage_ENSG	20	0.768549	-1.152	0.719722	3.210106	RP11-354E	Heart atria	GTEX_v6	T	C	73762673	10	rs2219837	0.039279	0.142675	ENSG00000272627.1
rs3180	Small_intestine_terminal_ilium	20	0.234035	1.160	0.719869	3.234679	MICU1	Small intes	GTEX_v6	T	C	73762673	10	rs2219837	-0.03956	0.142133	ENSG00000107745.12
rs7814941	Adipose_subcutaneous_ENSG0	20	0.683627	0.714	0.719958	1.992382	RP11-473C	Adipose su	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.031715	0.142686	ENSG00000253720.1
rs3180	Colon_transverse_ENSG00000	20	0.146298	-0.483	0.721051	1.353425	ANAPC16	Colon tran	GTEX_v6	T	C	73762673	10	rs2219837	0.016479	0.141902	ENSG00000166295.4
rs3180	Adipose_viscerl_omentum_E	20	0.987518	0.457	0.721159	1.279793	MCU	Adipose vi	GTEX_v6	T	C	73762673	10	rs2219837	-0.01558	0.141874	ENSG00000156026.10
rs3180	Breast_mammary_tissue_ENSG	5	0.02565	-1.725	0.721411	4.838453	RP11-152N	Breast mai	GTEX_v6	C	T	73899093	10	rs1245515	0.03209	0.142191	ENSG00000272599.1
rs3180	Artery_coronary_ENSG000002	1	NA	-2.291	0.72171	6.430922	RP11-152N	Artery cor	GTEX_v6	C	G	74046191	10	rs1074039	-0.03825	0.142084	ENSG00000227540.1
rs3180	Heart_left_ventricle_ENSG000	20	0.976855	-0.468	0.725831	1.335256	CHST3	Heart left	GTEX_v6	T	C	73762673	10	rs2219837	0.015967	0.139076	ENSG00000122863.5
rs7814941	Skin_not_sun_exposed_suprapu	20	0.367931	0.595	0.726721	1.703175	RP11-473C	Skin not su	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.026429	0.138513	ENSG00000254317.1
rs3180	Brain_anterior_cingulate_cort	20	0.295367	-1.726	0.728869	4.978672	UNC5B-AS	Brain ante	GTEX_v6	T	C	73762673	10	rs2219837	0.058849	0.136677	ENSG00000237512.2
rs3180	Esophagus_muscularis_ENSG0	1	NA	1.801	0.729237	5.204076	DNAJC9-A	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.030082	0.137729	ENSG00000236756.4
rs3180	Pancreas_ENSG00000182180.	1	NA	-1.423	0.730618	4.132952	MRPS16	Pancreas	GTEX_v6	C	G	74046191	10	rs1074039	-0.02376	0.136748	ENSG00000182180.9
rs3180	Brain_caudate_basal_ganglia_E	20	0.551083	-0.952	0.730667	2.765426	PSAP	Brain caud	GTEX_v6	T	C	73762673	10	rs2219837	0.032462	0.135918	ENSG00000197746.9
rs3180	Cells_EBV-transformed_lympho	8	0.312474	-1.888	0.731913	5.509639	RP11-344N	Cells EBV-t	GTEX_v6	T	C	73865131	10	rs1100017	0.035108	0.135676	ENSG00000272630.1
rs7814941	Skin_not_sun_exposed_suprapu	20	0.315172	-0.847	0.732199	2.473875	RP11-473C	Skin not su	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.03759	0.135249	ENSG00000243402.1
rs3180	Artery_tibial_ENSG000001383	20	0.400968	0.463	0.732439	1.354915	ASCC1	Artery tibi	GTEX_v6	T	C	73762673	10	rs2219837	-0.0158	0.135238	ENSG00000138303.13
rs3180	Spleen_ENSG00000138315.8	20	0.551846	1.518	0.733912	4.46624	OIT3	Spleen	GTEX_v6	T	C	73762673	10	rs2219837	-0.05177	0.133907	ENSG00000138315.8
rs7814941	Esophagus_muscularis_ENSG0	20	0.919479	0.754	0.734132	2.220193	RP11-473C	Esophagus	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.03348	0.134137	ENSG00000254317.1
rs3180	Brain_nucleus_accumbens_basi	20	0.499208	-1.064	0.734346	3.135577	SLC29A3	Brain nucle	GTEX_v6	T	C	73762673	10	rs2219837	0.036282	0.133678	ENSG00000198246.7
rs3180	Small_intestine_terminal_ilium	8	0.74881	2.225	0.734898	6.571806	RP11-344N	Small intest	GTEX_v6	T	C	73865131	10	rs1100017	-0.04139	0.133586	ENSG00000272630.1
rs3180	Pancreas_ENSG00000166321.	6	0.32516	-1.506	0.736135	4.469896	NUDT13	Pancreas	GTEX_v6	G	A	73883196	10	rs1245578	0.028016	0.133239	ENSG00000166321.9
rs3180	Brain_hypothalamus_ENSG000	8	0.762362	-1.981	0.736259	5.881809	P4HA1	Brain hypc	GTEX_v6	T	C	73858549	10	rs1668156	0.037046	0.132824	ENSG00000122884.8
rs7814941	Brain_putamen_basal_ganglia_	18	0.096669	0.664	0.736341	1.970901	ASAP1	Brain puta	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.029464	0.132368	ENSG00000153317.10
rs12310519	Ovary_ENSG00000255864.1	11	0.481087	-1.084	0.736712	3.22498	RP11-444E	Ovary	GTEX_v6	C	T	23982559	12	rs904988	0.06278	0.132177	ENSG00000255864.1
rs3180	Brain_frontal_cortex_BA9_ENS	20	0.287875	1.275	0.737011	3.797004	CDH23	Brain front	GTEX_v6	T	C	73762673	10	rs2219837	-0.04348	0.132108	ENSG00000107736.15
rs3180	Brain_anterior_cingulate_cort	8	0.880645	2.874	0.737625	8.579433	RP11-344N	Brain ante	GTEX_v6	T	C	73865131	10	rs1100017	-0.05346	0.131895	ENSG00000272630.1
rs3180	Thyroid_ENSG00000166228.4	2	NA	0.672	0.737627	2.00476	PCBD1	Thyroid	GTEX_v6	C	T	73646408	10	rs1437267	0.014708	0.132639	ENSG00000166228.4
rs3180	Artery_tibial_ENSG000001560	20	0.621116	-0.442	0.738505	1.324023	MCU	Artery tibi	GTEX_v6	T	C	73762673	10	rs2219837	0.015072	0.131648	ENSG00000156026.10
rs3180	Liver_ENSG00000148719.10	20	0.675503	-1.149	0.738718	3.445015	DNAJB12	Liver	GTEX_v6	T	C	73762673	10	rs2219837	0.039184	0.131145	ENSG00000148719.10
rs3180	Spleen_ENSG00000213551.4	1	NA	2.261	0.739112	6.788621	DNAJC9	Spleen	GTEX_v6	C	G	74046191	10	rs1074039	0.037756	0.131415	ENSG00000213551.4
rs3180	Adipose_viscerl_omentum_E	20	0.179096	-0.551	0.741985	1.67376	C10orf54	Adipose vi	GTEX_v6	T	C	73762673	10	rs2219837	0.018791	0.129495	ENSG00000107738.15
rs7814941	Esophagus_muscularis_ENSG0	20	0.70335	0.346	0.742272	1.052905	FAM49B	Esophagus	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.015373	0.129344	ENSG00000153310.14
rs3180	Cells_EBV-transformed_lympho	1	NA	1.888	0.742461	5.746447	ECD	Cells EBV-t	GTEX_v6	C	G	74046191	10	rs1074039	0.031534	0.129596	ENSG00000122882.6
rs3180	Testis_ENSG00000107731.8	20	0.942076	0.719	0.742857	2.19225	UNC5B	Testis	GTEX_v6	T	C	73762673	10	rs2219837	-0.02453	0.128924	ENSG00000107731.8
rs12310519	Lung_ENSG00000134532.11	11	0.117658	-0.334	0.743536	1.022114	SOX5	Lung	GTEX_v6	C	T	23982559	12	rs904988	0.019362	0.128641	ENSG00000134532.11
rs3180	Esophagus_mucosa_ENSG000	1	NA	-0.988	0.744164	3.028858	ECD	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	-0.01651	0.128827	ENSG00000122882.6
rs3180	Adipose_viscerl_omentum_E	5	0.648003	1.949	0.744221	5.972121	SNORA11	Adipose vi	GTEX_v6	C	T	73899093	10	rs1245515	-0.03624	0.128541	ENSG00000221164.1
rs3180	Esophagus_mucosa_ENSG000	8	0.757844	-1.333	0.744877	4.095169	RP11-344N	Esophagus	GTEX_v6	T	C	73865131	10	rs1100017	0.024786	0.128229	ENSG00000272630.1
rs3180	Brain_cerebellar_hemisphere_	2	NA	-1.561	0.745414	4.806134	PCBD1	Brain cere	GTEX_v6	C	T	73646408	10	rs1437267	-0.03418	0.1276	ENSG00000166228.4
rs3180	Brain_hypothalamus_ENSG000	20	0.504577	1.425	0.74565	4.393544	MICU1	Brain hypc	GTEX_v6	T	C	73762673	10	rs2219837	-0.0486	0.126952	ENSG00000107745.12
rs3180	Liver_ENSG00000107742.8	20	0.322845	1.159	0.74624	3.580677	SPOCK2	Liver	GTEX_v6	T	C	73762673	10	rs2219837	-0.03951	0.126751	ENSG00000107742.8
rs3180	Lung_ENSG00000156026.10	20	0.173207	-0.448	0.746856	1.386792	MCU	Lung	GTEX_v6	T	C	73762673	10	rs2219837	0.015265	0.12675	ENSG00000156026.10

rs3180	Cells transformed fibroblasts_	20	0.187428	0.407	0.746883	1.259649	UNC5B	Cells trans	GTEX_v6	T	C	73762673	10	rs2219837	-0.01386	0.12673	ENSG00000107731.8
rs3180	Brain nucleus accumbens basi	6	0.236733	2.125	0.747146	6.592319	NUDT13	Brain nucle	GTEX_v6	G	A	73883196	10	rs1245578	-0.03953	0.126535	ENSG00000166321.9
rs7814941	Skin sun exposed lower leg_EI	20	0.778753	0.689	0.747726	2.142413	RP11-473C	Skin sun e	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.030595	0.126228	ENSG00000243402.1
rs3180	Esophagus mucosa_ENSG00001	1	NA	1.741	0.748117	5.421998	EIF4A2P2	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.029077	0.126497	ENSG00000227382.1
rs3180	Vagina_ENSG00000107731.8	20	0.819609	0.854	0.748896	2.66891	UNC5B	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	-0.02913	0.12506	ENSG00000107731.8
rs3180	Colon sigmoid_ENSG0000016	2	NA	-1.212	0.749622	3.797233	PCBD1	Colon sigm	GTEX_v6	C	T	73646408	10	rs1437267	-0.02654	0.125335	ENSG00000166228.4
rs7814941	Brain hypothalamus_ENSG000	17	0.297761	1.079	0.750305	3.39121	RP11-473C	Brain hypc	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.047917	0.124228	ENSG00000253720.1
rs3180	Brain caudate basal ganglia_E	1	NA	-1.344	0.750583	4.229383	FAM149B1	Brain caud	GTEX_v6	C	G	74046191	10	rs1074039	-0.02245	0.124743	ENSG00000138286.10
rs3180	Brain putamen basal ganglia_	6	0.642506	-2.457	0.751253	7.751139	NUDT13	Brain puta	GTEX_v6	G	A	73883196	10	rs1245578	0.0457	0.124043	ENSG00000166321.9
rs3180	Liver_ENSG00000182180.9	1	NA	1.047	0.75135	3.302939	MRPS16	Liver	GTEX_v6	C	G	74046191	10	rs1074039	0.017478	0.124276	ENSG00000182180.9
rs3180	Muscle skeletal_ENSG000002	20	0.85271	-0.725	0.751619	2.290517	C10orf105	Muscle ske	GTEX_v6	T	C	73762673	10	rs2219837	0.024721	0.124027	ENSG00000214688.4
rs3180	Adipose subcutaneous_ENSG	6	0.583296	1.173	0.752382	3.716894	NUDT13	Adipose su	GTEX_v6	G	A	73883196	10	rs1245578	-0.02181	0.123873	ENSG00000166321.9
rs3180	Artery coronary_ENSG000001	20	0.488885	0.878	0.753616	2.796752	DDIT4	Artery cori	GTEX_v6	T	C	73762673	10	rs2219837	-0.02993	0.122597	ENSG00000168209.4
rs3180	Skin sun exposed lower leg_EI	20	0.524872	-0.606	0.753935	1.933258	CDH23	Skin sun e	GTEX_v6	T	C	73762673	10	rs2219837	0.020664	0.12266	ENSG00000107736.15
rs3180	Thyroid_ENSG00000166321.9	6	0.648536	0.988	0.755683	3.174671	NUDT13	Thyroid	GTEX_v6	G	A	73883196	10	rs1245578	-0.01837	0.121944	ENSG00000166321.9
rs3180	Adipose subcutaneous_ENSG	20	0.610093	-0.318	0.756697	1.025445	PSAP	Adipose su	GTEX_v6	T	C	73762673	10	rs2219837	0.010834	0.121067	ENSG00000197746.9
rs7814941	Uterus_ENSG00000254317.1	16	0.366078	-1.026	0.757158	3.316849	RP11-473C	Uterus	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.04554	0.120168	ENSG00000254317.1
rs3180	Small intestine terminal ileum	20	0.106223	0.733	0.757778	2.375891	MCU	Small intes	GTEX_v6	T	C	73762673	10	rs2219837	-0.02499	0.119922	ENSG00000156026.10
rs3180	Small intestine terminal ileum	5	0.768778	-3.306	0.758142	10.73664	SNORA11	Small intes	GTEX_v6	C	T	73899093	10	rs1245515	0.061492	0.120006	ENSG00000221164.1
rs3180	Artery aorta_ENSG000001228	1	NA	-1.209	0.759485	3.950584	ECD	Artery aori	GTEX_v6	C	G	74046191	10	rs1074039	-0.0202	0.119815	ENSG00000122882.6
rs12310519	Adipose visceral omentum_E	11	0.291238	0.445	0.762872	1.474888	SOX5	Adipose visi	GTEX_v6	C	T	23982559	12	rs9804988	-0.02577	0.117394	ENSG00000134532.11
rs3180	Brain hypothalamus_ENSG000	6	0.215986	-2.464	0.763715	8.196043	NUDT13	Brain hypc	GTEX_v6	G	A	73883196	10	rs1245578	0.045826	0.11686	ENSG00000166321.9
rs3180	Colon transverse_ENSG0000	1	NA	-1.647	0.76381	5.480343	RP11-152I	Colon tran	GTEX_v6	C	G	74046191	10	rs1074039	-0.0275	0.117275	ENSG00000227540.1
rs3180	Brain putamen basal ganglia_	20	0.295134	-1.082	0.764183	3.605874	DDIT4	Brain puta	GTEX_v6	T	C	73762673	10	rs2219837	0.036887	0.116334	ENSG00000168209.4
rs7814941	Brain hippocampus_ENSG000	17	0.275381	-0.714	0.764425	2.38138	FAM49B	Brain hipp	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.03169	0.116163	ENSG00000153310.14
rs3180	Brain nucleus accumbens basi	1	NA	1.817	0.765029	6.078338	DNAJC9	Brain nuckl	GTEX_v6	C	G	74046191	10	rs1074039	0.030339	0.116345	ENSG00000213551.4
rs3180	Brain hypothalamus_ENSG000	1	NA	-2.118	0.765544	7.101776	ECD	Brain hypc	GTEX_v6	C	G	74046191	10	rs1074039	-0.03537	0.11595	ENSG00000122882.6
rs3180	Vagina_ENSG00000107745.12	20	0.092989	0.847	0.768236	2.874267	MICU1	Vagina	GTEX_v6	T	C	73762673	10	rs2219837	-0.02888	0.114024	ENSG00000107745.12
rs3180	Brain anterior cingulate cortex	1	NA	2.425	0.768272	8.231251	DNAJC9-A'	Brain ante	GTEX_v6	C	G	74046191	10	rs1074039	0.040501	0.114291	ENSG00000236756.4
rs3180	Brain frontal cortex BA9_ENS	5	0.260562	2.528	0.768753	8.599735	RP11-152I	Brain front	GTEX_v6	C	T	73899093	10	rs1245515	-0.04703	0.114087	ENSG00000272599.1
rs3180	Adrenal gland_ENSG00000238	1	NA	1.858	0.769062	6.327849	DNAJC9-A'	Adrenal gl	GTEX_v6	C	G	74046191	10	rs1074039	0.031026	0.11142	ENSG00000236756.4
rs3180	Esophagus mucosa_ENSG000	1	NA	1.546	0.76944	5.273657	DNAJC9-A'	Esophagus	GTEX_v6	C	G	74046191	10	rs1074039	0.025814	0.114146	ENSG00000236756.4
rs3180	Spleen_ENSG00000227540.1	1	NA	2.538	0.772754	8.789621	RP11-152I	Spleen	GTEX_v6	C	G	74046191	10	rs1074039	0.042388	0.111922	ENSG00000227540.1
rs7814941	Adipose visceral omentum_E	20	0.287987	-0.564	0.7732	1.956558	RP11-473C	Adipose vi	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.02504	0.111567	ENSG00000254263.1
rs7814941	Brain cerebellum_ENSG0000	18	0.915547	0.482	0.773484	1.673271	FAM49B	Brain cere	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.021383	0.11122	ENSG00000153310.14
rs3180	Brain caudate basal ganglia_E	1	NA	1.154	0.773981	4.01744	ECD	Brain caud	GTEX_v6	C	G	74046191	10	rs1074039	0.019267	0.111299	ENSG00000122882.6
rs7814941	Heart left ventricle_ENSG000	19	0.707034	-0.437	0.774765	1.528795	ASAP1	Heart left \v	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.01942	0.110696	ENSG00000153317.10
rs3180	Muscle skeletal_ENSG000001	20	0.517242	-0.420	0.774861	1.467046	UNC5B	Muscle ske	GTEX_v6	T	C	73762673	10	rs2219837	0.014309	0.110775	ENSG00000107731.8
rs12310519	Lung_ENSG00000255864.1	11	0.928339	0.432	0.775559	1.514969	RP11-444C	Lung	GTEX_v6	C	T	23982559	12	rs9804988	-0.02501	0.110301	ENSG00000255864.1
rs12310519	Testis_ENSG00000255864.1	11	0.676763	-0.875	0.777131	3.090584	RP11-444C	Testis	GTEX_v6	C	T	23982559	12	rs9804988	0.050652	0.109306	ENSG00000255864.1
rs3180	Pituitary_ENSG00000227382..	1	NA	-2.983	0.778309	10.59741	EIF4A2P2	Pituitary	GTEX_v6	C	G	74046191	10	rs1074039	-0.04982	0.108777	ENSG00000227382.1
rs7814941	Brain cortex_ENSG000001533	18	0.714715	-0.305	0.77834	1.085105	FAM49B	Brain cort	GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.01356	0.108471	ENSG00000153310.14
rs3180	Thyroid_ENSG00000213551.4	1	NA	1.090	0.778517	3.873915	DNAJC9	Thyroid	GTEX_v6	C	G	74046191	10	rs1074039	0.018195	0.109023	ENSG00000213551.4
rs3180	Heart left ventricle_ENSG000	1	NA	-1.279	0.778691	4.551679	DNAJC9	Heart left \v	GTEX_v6	C	G	74046191	10	rs1074039	-0.02136	0.10885	ENSG00000213551.4
rs3180	Adipose subcutaneous_ENSG	2	NA	-0.765	0.778962	2.724333	PCBD1	Adipose su	GTEX_v6	C	T	73646408	10	rs1437267	-0.01675	0.108726	ENSG00000166228.4
rs7814941	Brain putamen basal ganglia_	18	0.97408	0.777	0.779929	2.780934	GSDMC	Brain puta	GTEX_v6	A	G	1.31E+08	8	rs1095648	0.0345	0.107486	ENSG00000147697.4
rs3180	Adrenal gland_ENSG0000010	20	0.982929	0.615	0.78052	2.207618	UNC5B	Adrenal gl	GTEX_v6	T	C	73762673	10	rs2219837	-0.02098	0.107403	ENSG00000107731.8
rs3180	Breast mammary tissue_ENSC	20	0.273959	0.829	0.780807	2.979069	UNC5B	Breast mai	GTEX_v6	T	C	73762673	10	rs2219837	-0.02827	0.107332	ENSG00000107731.8
rs3180	Brain hypothalamus_ENSG00	20	0.749513	-1.772	0.780944	6.371482	RP11-354E	Brain hypc	GTEX_v6	T	C	73762673	10	rs2219837	0.06042	0.106934	ENSG00000272627.1
rs3180	Pituitary_ENSG00000227540.	1	NA	-1.954	0.781031	7.029357	RP11-152I	Pituitary	GTEX_v6	C	G	74046191	10	rs1074039	-0.03263	0.107252	ENSG00000227540.1

rs3180	Esophagus mucosa_ENSG00001	20	0.974388	-0.724	0.781286	2.607733	RP11-354E	Esophagus GTEX_v6	T	C	73762673	10	rs2219837	0.024689	0.107128	ENSG00000272627.1
rs3180	Brain anterior cingulate cortex	1	NA	-1.694	0.781462	6.105407	ECD	Brain ante GTEX_v6	C	G	74046191	10	rs1074039	-0.02829	0.106865	ENSG00000122882.6
rs3180	Brain cortex_ENSG000002367	1	NA	2.181	0.781517	7.865186	DNAJC9-A	Brain cort GTEX_v6	C	G	74046191	10	rs1074039	0.036429	0.10704	ENSG00000236756.4
rs3180	Small intestine terminal ileum	2	NA	1.280	0.781919	4.622895	PCBD1	Small intes GTEX_v6	C	T	73646408	10	rs1437267	0.028026	0.106613	ENSG00000166228.4
rs3180	Brain anterior cingulate cortex	1	NA	2.951	0.782005	10.66336	EIF4A2P2	Brain ante GTEX_v6	C	G	74046191	10	rs1074039	0.049275	0.106562	ENSG00000227382.1
rs7814941	Brain hypothalamus_ENSG000	17	0.918905	-1.024	0.7836	3.727993	RP11-473C	Brain hypc GTEX_v6	A	G	1.31E+08	8	rs1095648	-0.04546	0.105446	ENSG00000254317.1
rs3180	Skin sun exposed lower leg_EI	1	NA	1.180	0.784107	4.306795	DNAJC9-A	Skin sun e GTEX_v6	C	G	74046191	10	rs1074039	0.019705	0.105898	ENSG00000236756.4
rs3180	Ovary_ENSG00000138315.8	20	0.578872	-1.274	0.784228	4.653134	OIT3	Ovary GTEX_v6	T	C	73762673	10	rs2219837	0.043446	0.10516	ENSG00000138315.8
rs12310519	Testis_ENSG00000256120.1	11	0.444793	-0.402	0.784568	1.469907	RP11-778P	Testis GTEX_v6	C	T	23982559	12	rs9804988	0.023266	0.105175	ENSG00000256120.1
rs3180	Adipose visceral omentum_EI	1	NA	-0.927	0.784871	3.395587	FAM149B1	Adipose vi GTEX_v6	C	G	74046191	10	rs1074039	-0.01548	0.10538	ENSG00000138286.10
rs3180	Brain nucleus accumbens basi	1	NA	-2.017	0.78539	7.405911	DNAJC9-A	Brain nuck GTEX_v6	C	G	74046191	10	rs1074039	-0.03368	0.104863	ENSG00000236756.4
rs3180	Adrenal gland_ENSG0000012	20	0.734983	-0.799	0.786013	2.943766	CHST3	Adrenal gl GTEX_v6	T	C	73762673	10	rs2219837	0.027253	0.10436	ENSG00000122863.5
rs3180	Vagina_ENSG00000138303.13	20	0.900566	-0.696	0.786159	2.56372	ASCC1	Vagina GTEX_v6	T	C	73762673	10	rs2219837	0.023718	0.104045	ENSG00000138303.13
rs7814941	Vagina_ENSG00000147697.4	17	0.502242	0.503	0.786475	1.858081	GSDMC	Vagina GTEX_v6	A	G	1.31E+08	8	rs1095648	0.022348	0.103854	ENSG00000147697.4
rs3180	Lung_ENSG00000198246.7	20	0.664339	-0.345	0.786658	1.274718	SLC29A3	Lung GTEX_v6	T	C	73762673	10	rs2219837	0.011765	0.10417	ENSG00000198246.7
rs3180	Esophagus gastroesophageal j	2	NA	1.045	0.786957	3.865063	PCBD1	Esophagus GTEX_v6	C	T	73646408	10	rs1437267	0.022877	0.104082	ENSG00000166228.4
rs3180	Cells transformed fibroblasts_	20	0.503694	-0.660	0.787984	2.455042	UNC5B-AS	Cells trans GTEX_v6	T	C	73762673	10	rs2219837	0.022514	0.103435	ENSG00000237512.2
rs3180	Brain cerebellum_ENSG00000	8	0.184038	1.852	0.788694	6.909718	RP11-344N	Brain cerel GTEX_v6	T	C	73865131	10	rs1100017	-0.03444	0.102987	ENSG00000272630.1
rs3180	Artery coronary_ENSG000001	20	0.750714	-0.641	0.789021	2.396632	MICU1	Artery cor GTEX_v6	T	C	73762673	10	rs2219837	0.021868	0.102679	ENSG00000107745.12
rs3180	Brain frontal cortex BA9_ENS	8	0.879302	1.143	0.789063	4.274245	P4HA1	Brain front GTEX_v6	T	C	73858549	10	rs1668156	-0.02138	0.102722	ENSG00000122884.8
rs3180	Liver_ENSG00000107731.8	20	0.464776	-0.968	0.789663	3.628678	UNC5B	Liver GTEX_v6	T	C	73762673	10	rs2219837	0.033007	0.102239	ENSG00000107731.8
rs3180	Prostate_ENSG00000227382..	1	NA	-2.606	0.791402	9.851837	EIF4A2P2	Prostate GTEX_v6	C	G	74046191	10	rs1074039	-0.04352	0.101501	ENSG00000227382.1
rs12310519	Skin not sun exposed suprapu	11	0.87361	-0.378	0.792134	1.43341	RP11-444E	Skin not su GTEX_v6	C	T	23982559	12	rs9804988	0.021872	0.101071	ENSG00000255864.1
rs7814941	Lung_ENSG00000153310.14	20	0.273103	0.231	0.792676	0.877567	FAM49B	Lung GTEX_v6	A	G	1.31E+08	8	rs1095648	0.010241	0.100842	ENSG00000153310.14
rs3180	Brain hippocampus_ENSG000	1	NA	-1.854	0.79383	7.094445	ECD	Brain hipp GTEX_v6	C	G	74046191	10	rs1074039	-0.03096	0.100112	ENSG00000122882.6
rs3180	Colon transverse_ENSG00000	20	0.777687	0.496	0.795429	1.912941	PSAP	Colon tran GTEX_v6	T	C	73762673	10	rs2219837	-0.01691	0.099253	ENSG00000197746.9
rs3180	Lung_ENSG00000182180.9	1	NA	-0.344	0.795431	1.327647	MRPS16	Lung GTEX_v6	C	G	74046191	10	rs1074039	-0.00575	0.099604	ENSG00000182180.9
rs3180	Brain frontal cortex BA9_ENS	20	0.577092	-0.830	0.795513	3.204099	C10orf105	Brain front GTEX_v6	T	C	73762673	10	rs2219837	0.028316	0.099013	ENSG000002146884.4
rs3180	Uterus_ENSG00000148719.1C	20	0.139402	-1.003	0.796512	3.891529	DNAJB12	Uterus GTEX_v6	T	C	73762673	10	rs2219837	0.034219	0.098293	ENSG00000148719.10
rs3180	Adipose subcutaneous_ENSG	20	0.137654	0.497	0.796599	1.926941	UNC5B	Adipose su GTEX_v6	T	C	73762673	10	rs2219837	-0.01694	0.098722	ENSG00000107731.8
rs3180	Vagina_ENSG00000272599.1	5	0.4536	-2.070	0.796727	8.036108	RP11-152N	Vagina GTEX_v6	C	T	73899093	10	rs1245515	0.038502	0.098432	ENSG00000272599.1
rs3180	Adipose subcutaneous_ENSG	20	0.540989	-0.594	0.797078	2.310102	RP11-570C	Adipose su GTEX_v6	T	C	73762673	10	rs2219837	0.020255	0.09846	ENSG00000226701.1
rs3180	Breast mammary tissue_ENS	20	0.498135	-0.579	0.798041	2.261949	SLC29A3	Breast mai GTEX_v6	T	C	73762673	10	rs2219837	0.019733	0.097851	ENSG00000198246.7
rs3180	Pancreas_ENSG00000237512.	20	0.750025	-0.911	0.799028	3.5765	UNC5B-AS	Pancreas GTEX_v6	T	C	73762673	10	rs2219837	0.031051	0.097256	ENSG00000237512.2
rs12310519	Brain caudate basal ganglia_E	11	0.103392	-0.335	0.800124	1.324042	SOX5	Brain caud GTEX_v6	C	T	23982559	12	rs9804988	0.01941	0.096531	ENSG00000134532.11
rs3180	Adipose visceral omentum_EI	20	0.286927	0.616	0.800128	2.434923	UNC5B	Adipose vi GTEX_v6	T	C	73762673	10	rs2219837	-0.02102	0.096721	ENSG00000107731.8
rs3180	Spleen_ENSG00000107731.8	20	0.359192	0.687	0.800385	2.716858	UNC5B	Spleen GTEX_v6	T	C	73762673	10	rs2219837	-0.02343	0.096351	ENSG00000107731.8
rs3180	Brain cerebellum_ENSG00000	1	NA	2.135	0.805354	8.663252	EIF4A2P2	Brain cerel GTEX_v6	C	G	74046191	10	rs1074039	0.035652	0.093957	ENSG00000227382.1
rs3180	Stomach_ENSG00000138303.	20	0.043339	0.436	0.806292	1.776769	ASCC1	Stomach GTEX_v6	T	C	73762673	10	rs2219837	-0.01486	0.093368	ENSG00000138303.13
rs3180	Artery coronary_ENSG000002	1	NA	-2.009	0.806351	8.196657	DNAJC9-A	Artery cor GTEX_v6	C	G	74046191	10	rs1074039	-0.03356	0.093469	ENSG00000236756.4
rs3180	Spleen_ENSG00000272630.1	8	0.576864	-1.440	0.808067	5.928327	RP11-344N	Spleen GTEX_v6	T	C	73865131	10	rs1100017	0.026786	0.092352	ENSG00000272630.1
rs3180	Esophagus mucosa_ENSG000	6	0.304432	0.957	0.808123	3.942276	NUDT13	Esophagus GTEX_v6	G	A	73883196	10	rs1245578	-0.01781	0.092591	ENSG00000166321.9
rs3180	Heart atrial appendage_ENSG	20	0.38947	0.396	0.808811	1.635666	ANAPC16	Heart atria GTEX_v6	T	C	73762673	10	rs2219837	-0.0135	0.091995	ENSG00000166295.4
rs7814941	Spleen_ENSG00000153310.14	17	0.970277	0.438	0.810456	1.825043	FAM49B	Spleen GTEX_v6	A	G	1.31E+08	8	rs1095648	0.019435	0.090925	ENSG00000153310.14
rs7814941	Adipose visceral omentum_EI	20	0.422529	0.535	0.810546	2.232729	RP11-473C	Adipose vi GTEX_v6	A	G	1.31E+08	8	rs1095648	0.023764	0.091092	ENSG00000254317.1
rs3180	Heart left ventricle_ENSG000	20	0.790608	0.363	0.811662	1.52424	MICU1	Heart left GTEX_v6	T	C	73762673	10	rs2219837	-0.01239	0.090512	ENSG00000107745.12
rs12310519	Breast mammary tissue_ENS	11	0.544491	-0.307	0.812573	1.293241	SOX5	Breast mai GTEX_v6	C	T	23982559	12	rs9804988	0.017754	0.09	ENSG00000134532.11
rs3180	Cells EBV-transformed lymph	20	0.129155	0.997	0.812844	4.211382	Y_RNA	Cells EBV-t GTEX_v6	T	C	73762673	10	rs2219837	-0.034	0.089768	ENSG00000200170.1
rs7814941	Stomach_ENSG00000147697.	20	0.875984	0.647	0.813848	2.749072	GSDMC	Stomach GTEX_v6	A	G	1.31E+08	8	rs1095648	0.028741	0.089308	ENSG00000147697.4
rs3180	Liver_ENSG00000215086.2	20	0.064484	0.840	0.814024	3.571895	NPM1P24	Liver GTEX_v6	T	C	73762673	10	rs2219837	-0.02865	0.089076	ENSG00000215086.2

rs7814941	Colon sigmoid_ENSG0000025·	17	0.865259	-0.709	0.816759	3.059642	RP11-473C	Colon signr	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.03148	0.087702	ENSG00000254317.1
rs3180	Pituitary_ENSG00000237512.·	20	0.318054	-1.181	0.817482	5.115717	UNC5B-AS	Pituitary	GTEEx_v6	T	C	73762673	10	rs2219837	0.04026	0.087189	ENSG00000237512.2
rs3180	Lung_ENSG00000138303.13	20	0.083219	0.296	0.817508	1.282204	ASCC1	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	-0.01009	0.087455	ENSG00000138303.13
rs3180	Heart atrial appendage_ENSG	5	0.297172	1.365	0.81813	5.935137	RP11-152·	Heart atria	GTEEx_v6	C	T	73899093	10	rs1245515	-0.02539	0.087141	ENSG00000272599.1
rs3180	Brain putamen basal ganglia_	20	0.820781	1.310	0.818596	5.713602	RP11-354E	Brain puta	GTEEx_v6	T	C	73762673	10	rs2219837	-0.04469	0.086568	ENSG00000272627.1
rs3180	Adrenal gland_ENSG0000027·	5	0.147662	1.174	0.81895	5.130728	RP11-152·	Adrenal gl	GTEEx_v6	C	T	73899093	10	rs1245515	-0.02184	0.086669	ENSG00000272599.1
rs3180	Brain cortex_ENSG000001977	20	0.765815	0.714	0.819566	3.130362	PSAP	Brain cort	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02435	0.086134	ENSG00000197746.9
rs3180	Muscle skeletal_ENSG000002·	8	0.260139	0.845	0.819958	3.713222	RP11-344·	Muscle ske	GTEEx_v6	T	C	73865131	10	rs1100017	-0.01572	0.086293	ENSG00000272630.1
rs7814941	Colon transverse_ENSG00000	19	0.012157	-0.240	0.820022	1.056126	FAM49B	Colon tran	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.01067	0.086028	ENSG00000153310.14
rs3180	Esophagus muscularis_ENSG0	20	0.658167	0.348	0.820772	1.538047	PSAP	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.01188	0.085692	ENSG00000197746.9
rs3180	Brain frontal cortex_BA9_ENS	1	NA	-1.847	0.820922	8.161219	RP11-152·	Brain front	GTEEx_v6	C	G	74046191	10	rs1074039	-0.03085	0.085563	ENSG00000227540.1
rs3180	Esophagus muscularis_ENSG0	20	0.812576	0.689	0.82252	3.070686	RP11-354E	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02349	0.084767	ENSG00000272627.1
rs3180	Skin sun exposed lower leg_EI	1	NA	0.547	0.82363	2.455299	ECD	Skin sun e	GTEEx_v6	C	G	74046191	10	rs1074039	0.009139	0.08438	ENSG00000122882.6
rs3180	Esophagus mucosa_ENSG0000	20	0.542176	-0.415	0.825033	1.876384	UNC5B-AS	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	0.014146	0.083458	ENSG00000237512.2
rs3180	Esophagus muscularis_ENSG0	20	0.735773	-0.474	0.825577	2.148767	UNC5B	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	0.016148	0.083157	ENSG00000107731.8
rs7814941	Prostate_ENSG00000153310.·	18	0.440701	0.437	0.825622	1.983539	FAM49B	Prostate	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.019403	0.082897	ENSG00000153310.14
rs3180	Brain cerebellar hemisphere_	20	0.350782	0.686	0.825926	3.11795	ASCC1	Brain cere	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02338	0.082752	ENSG00000138303.13
rs3180	Small intestine terminal ileum	1	NA	2.263	0.826349	10.31665	DNAJC9-A'	Small intes	GTEEx_v6	C	G	74046191	10	rs1074039	0.037798	0.082603	ENSG00000236756.4
rs7814941	Lung_ENSG00000254263.1	20	0.874003	0.420	0.826767	1.91784	RP11-473C	Lung	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.018636	0.082553	ENSG00000254263.1
rs3180	Testis_ENSG00000223817.1	20	0.276762	-0.756	0.826832	3.455814	CDH23-AS	Testis	GTEEx_v6	T	C	73762673	10	rs2219837	0.02578	0.082434	ENSG00000223817.1
rs7814941	Vagina_ENSG00000153310.14	17	0.423103	0.303	0.829375	1.407232	FAM49B	Vagina	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.013465	0.080887	ENSG00000153310.14
rs3180	Brain hippocampus_ENSG000	1	NA	0.974	0.829509	4.523837	FAM149B1	Brain hipp	GTEEx_v6	C	G	74046191	10	rs1074039	0.016268	0.080973	ENSG00000138286.10
rs3180	Whole blood_ENSG00000122·	1	NA	0.404	0.830262	1.886278	ECD	Whole blo	GTEEx_v6	C	G	74046191	10	rs1074039	0.006753	0.080888	ENSG00000122882.6
rs3180	Brain hippocampus_ENSG000	20	0.257722	-0.550	0.830282	2.563791	UNC5B	Brain hipp	GTEEx_v6	T	C	73762673	10	rs2219837	0.018739	0.080429	ENSG00000107731.8
rs3180	Testis_ENSG00000272630.1	8	0.697194	-0.954	0.831523	4.485825	RP11-344·	Testis	GTEEx_v6	T	C	73865131	10	rs1100017	0.017751	0.08007	ENSG00000272630.1
rs3180	Cells transformed fibroblasts_	20	0.155721	-0.458	0.831903	2.156669	RP11-570C	Cells trans	GTEEx_v6	T	C	73762673	10	rs2219837	0.01561	0.079869	ENSG00000226701.1
rs3180	Lung_ENSG00000166228.4	2	NA	0.531	0.832567	2.510127	PCBD1	Lung	GTEEx_v6	C	T	73646408	10	rs1437267	0.011622	0.079635	ENSG00000166228.4
rs3180	Esophagus muscularis_ENSG0	20	0.756759	0.611	0.834598	2.927606	C10orf105	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.02085	0.078439	ENSG00000214688.4
rs3180	Esophagus gastroesophageal	20	0.107674	-0.475	0.834771	2.276589	CHST3	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	0.016193	0.07826	ENSG00000122863.5
rs3180	Nerve tibial_ENSG000002375·	20	0.422005	-0.569	0.835341	2.736705	UNC5B-AS	Nerve tibi	GTEEx_v6	T	C	73762673	10	rs2219837	0.019398	0.078071	ENSG00000237512.2
rs7814941	Brain nucleus accumbens basa	18	0.177034	0.777	0.83678	3.769855	RP11-473C	Brain nucle	GTEEx_v6	A	G	1.31E+08	8	rs1095648	0.034483	0.077112	ENSG00000253720.1
rs3180	Artery coronary_ENSG000001	1	NA	-1.138	0.838369	5.578431	ECD	Artery coro	GTEEx_v6	C	G	74046191	10	rs1074039	-0.019	0.076495	ENSG00000122882.6
rs3180	Whole blood_ENSG00000122·	20	0.33015	-0.332	0.839297	1.635592	CHST3	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	0.011311	0.076047	ENSG00000122863.5
rs3180	Cells EBV-transformed lympho	20	0.560504	-0.536	0.839514	2.648171	SLC29A3	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	0.018288	0.075775	ENSG00000198246.7
rs3180	Cells transformed fibroblasts_	20	0.971799	-0.280	0.83954	1.384398	C10orf54	Cells trans	GTEEx_v6	T	C	73762673	10	rs2219837	0.009559	0.075901	ENSG00000107738.15
rs3180	Stomach_ENSG00000122863.	20	0.248621	0.417	0.840384	2.070122	CHST3	Stomach	GTEEx_v6	T	C	73762673	10	rs2219837	-0.01422	0.075397	ENSG00000122863.5
rs3180	Brain hypothalamus_ENSG000	1	NA	-0.936	0.840453	4.651601	FAM149B1	Brain hypc	GTEEx_v6	C	G	74046191	10	rs1074039	-0.01564	0.075276	ENSG00000138286.10
rs3180	Brain hypothalamus_ENSG000	1	NA	0.928	0.840771	4.619791	DNAJC9-A'	Brain hypc	GTEEx_v6	C	G	74046191	10	rs1074039	0.0155	0.075112	ENSG00000236756.4
rs12310519	Skin sun exposed lower leg_EI	11	0.18234	0.207	0.845744	1.06587	SOX5	Skin sun e	GTEEx_v6	C	T	23982559	12	rs9804988	-0.01201	0.072705	ENSG00000134532.11
rs3180	Colon transverse_ENSG00000	8	0.53797	-0.988	0.846069	5.089257	RP11-344·	Colon tran	GTEEx_v6	T	C	73865131	10	rs1100017	0.018377	0.072539	ENSG00000272630.1
rs3180	Colon transverse_ENSG00000	20	0.57324	-0.278	0.846421	1.433013	PLA2G12B	Colon tran	GTEEx_v6	T	C	73762673	10	rs2219837	0.009465	0.072291	ENSG00000138308.5
rs3180	Breast mammary tissue_ENSG	5	0.572047	-1.092	0.846434	5.637583	SNORA11	Breast mai	GTEEx_v6	C	T	73899093	10	rs1245515	0.020308	0.072366	ENSG00000221164.1
rs3180	Spleen_ENSG00000236756.4	1	NA	2.053	0.846758	10.621233	DNAJC9-A'	Spleen	GTEEx_v6	C	G	74046191	10	rs1074039	0.034279	0.07207	ENSG00000236756.4
rs3180	Lung_ENSG00000107736.15	20	0.38933	0.416	0.847371	2.161947	CDH23	Lung	GTEEx_v6	T	C	73762673	10	rs2219837	-0.01419	0.071871	ENSG00000107736.15
rs7814941	Nerve tibial_ENSG000002537·	20	0.592699	-0.415	0.847703	2.158357	RP11-473C	Nerve tibi	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.0184	0.071687	ENSG00000253720.1
rs3180	Lung_ENSG00000227540.1	1	NA	0.681	0.848337	3.55984	RP11-152·	Lung	GTEEx_v6	C	G	74046191	10	rs1074039	0.011369	0.071473	ENSG00000227540.1
rs3180	Brain frontal cortex_BA9_ENS	1	NA	-0.835	0.848714	4.375052	DNAJC9	Brain front	GTEEx_v6	C	G	74046191	10	rs1074039	-0.01394	0.071081	ENSG00000213551.4
rs3180	Heart left ventricle_ENSG0000	1	NA	0.717	0.849147	3.769519	FAM149B1	Heart left	GTEEx_v6	C	G	74046191	10	rs1074039	0.011974	0.071012	ENSG00000138286.10
rs3180	Nerve tibial_ENSG000002003·	1	NA	1.140	0.850398	6.045935	RNU6-833	Nerve tibi	GTEEx_v6	C	G	74046191	10	rs1074039	0.019044	0.070407	ENSG00000200356.1
rs3180	Adipose subcutaneous_ENSG(1	NA	-0.738	0.85076	3.925011	DNAJC9-A'	Adipose su	GTEEx_v6	C	G	74046191	10	rs1074039	-0.01233	0.070236	ENSG00000236756.4

rs3180	Esophagus mucosa_ENSG0000198246.7	20	0.564434	0.420	0.851008	2.234679	SLC29A3	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	-0.01431	0.069998	ENSG00000198246.7
rs3180	Brain cortex_ENSG0000018210.9	1	NA	-1.003	0.854735	5.479058	MRPS16	Brain corte GTEx_v6	C	G	74046191	10	rs1074039	-0.01675	0.068024	ENSG0000018210.9
rs12310519	Cells EBV-transformed lympho	11	0.317932	0.405	0.855733	2.226635	SOX5	Cells EBV-t GTEx_v6	C	T	23982559	12	rs9804988	-0.02344	0.067476	ENSG00000134532.11
rs3180	Muscle skeletal_ENSG00000227540.1	1	NA	0.675	0.858188	3.377922	RP11-152N	Muscle ske GTEx_v6	C	G	74046191	10	rs1074039	0.011277	0.066462	ENSG00000227540.1
rs3180	Stomach_ENSG00000156026.10	20	0.814631	0.182	0.858189	1.015916	MCU	Stomach GTEx_v6	T	C	73762673	10	rs2219837	-0.00619	0.066303	ENSG00000156026.10
rs3180	Heart left ventricle_ENSG0000138303.13	20	0.181919	-0.251	0.858735	1.407733	ASCC1	Heart left\ GTEx_v6	T	C	73762673	10	rs2219837	0.008544	0.066045	ENSG00000138303.13
rs7814941	Artery coronary_ENSG00000153310.14	19	0.288691	0.226	0.85966	1.279199	FAM49B	Artery coro GTEx_v6	A	G	1.31E+08	8	rs1095648	0.010042	0.065503	ENSG00000153310.14
rs3180	Brain putamen basal ganglia_	20	0.244917	-0.596	0.861971	3.425761	C10orf105	Brain puta GTEx_v6	T	C	73762673	10	rs2219837	0.020311	0.064233	ENSG00000214688.4
rs3180	Adipose visceral omentum_EI	1	NA	0.711	0.862449	4.102535	RP11-152M	Adipose vi GTEx_v6	C	G	74046191	10	rs1074039	0.01187	0.06424	ENSG00000227540.1
rs3180	Artery aorta_ENSG00000227382.1	1	NA	-1.213	0.862533	7.003429	EIF4A2P2	Artery aor GTEx_v6	C	G	74046191	10	rs1074039	-0.02025	0.064207	ENSG00000227382.1
rs3180	Whole blood_ENSG0000023751.2	20	0.169728	-0.389	0.862779	2.249049	UNC5B-AS	Whole blo GTEx_v6	T	C	73762673	10	rs2219837	0.013255	0.064062	ENSG0000023751.2
rs3180	Breast mammary tissue_ENSG	1	NA	0.397	0.863061	2.304584	MRPS16	Breast mai GTEx_v6	C	G	74046191	10	rs1074039	0.006638	0.063929	ENSG00000182180.9
rs12310519	Liver_ENSG00000255864.1	11	0.63487	-0.541	0.863426	3.145896	RP11-444L	Liver GTEx_v6	C	T	23982559	12	rs9804988	0.031332	0.063557	ENSG00000255864.1
rs3180	Thyroid_ENSG00000107736.15	20	0.83603	0.313	0.863558	1.818581	CDH23	Thyroid GTEx_v6	T	C	73762673	10	rs2219837	-0.01066	0.063655	ENSG00000107736.15
rs3180	Esophagus muscularis_ENSG0	20	0.313428	-0.249	0.864871	1.46225	C10orf54	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	0.008486	0.062973	ENSG00000107738.15
rs3180	Adrenal gland_ENSG00000107736.15	20	0.358577	-0.491	0.864997	2.890085	CDH23	Adrenal gl GTEx_v6	T	C	73762673	10	rs2219837	0.016756	0.06284	ENSG00000107736.15
rs3180	Pancreas_ENSG00000272630.1	8	0.933858	1.008	0.865299	5.943386	RP11-344N	Pancreas GTEx_v6	T	C	73865131	10	rs1100017	-0.01875	0.062744	ENSG00000272630.1
rs3180	Esophagus muscularis_ENSG0	20	0.94746	-0.234	0.865885	1.3861	SLC29A3	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	0.007983	0.062465	ENSG00000198246.7
rs3180	Liver_ENSG00000122884.8	8	0.683025	-1.180	0.866563	7.024504	P4HA1	Liver GTEx_v6	T	C	73858549	10	rs1668156	0.022072	0.062035	ENSG00000122884.8
rs3180	Esophagus gastroesophageal j	20	0.398838	-0.383	0.866668	2.282876	DNAJB12	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	0.01307	0.062005	ENSG00000148719.10
rs3180	Brain hippocampus_ENSG000	20	0.525636	0.336	0.866707	2.003677	CHST3	Brain hippoc GTEx_v6	T	C	73762673	10	rs2219837	-0.01147	0.061859	ENSG00000122863.5
rs3180	Breast mammary tissue_ENSG	20	0.976452	-0.571	0.866962	3.404917	NPM1P24	Breast mai GTEx_v6	T	C	73762673	10	rs2219837	0.019456	0.061924	ENSG00000215086.2
rs3180	Brain hippocampus_ENSG000	1	NA	-1.959	0.867428	11.737	EIF4A2P2	Brain hippoc GTEx_v6	C	G	74046191	10	rs1074039	-0.03272	0.061563	ENSG00000227382.1
rs3180	Brain caudate basal ganglia_E	5	0.152039	-1.510	0.868205	9.101683	RP11-152N	Brain caud GTEx_v6	C	T	73899093	10	rs1245515	0.028092	0.061223	ENSG00000272599.1
rs3180	Skin sun exposed lower leg_EI	5	0.193787	0.633	0.869497	3.851458	RP11-152N	Skin sun ex GTEx_v6	C	T	73899093	10	rs1245515	-0.01177	0.060726	ENSG00000272599.1
rs3180	Spleen_ENSG00000215086.2	20	0.584497	-0.786	0.869561	4.78843	NPM1P24	Spleen GTEx_v6	T	C	73762673	10	rs2219837	0.026814	0.060471	ENSG00000215086.2
rs3180	Brain frontal cortex_BA9_ENSG	20	0.261626	0.536	0.870063	3.277797	MCU	Brain front GTEx_v6	T	C	73762673	10	rs2219837	-0.01828	0.060232	ENSG00000156026.10
rs3180	Uterus_ENSG00000182180.9	1	NA	-0.586	0.870575	3.597654	MRPS16	Uterus GTEx_v6	C	G	74046191	10	rs1074039	-0.00979	0.059935	ENSG00000182180.9
rs3180	Testis_ENSG00000214688.4	20	0.673643	0.276	0.871354	1.704778	C10orf105	Testis GTEx_v6	T	C	73762673	10	rs2219837	-0.00941	0.059688	ENSG00000214688.4
rs3180	Colon sigmoid_ENSG00000227382.1	1	NA	1.298	0.871479	8.020912	EIF4A2P2	Colon sigm GTEx_v6	C	G	74046191	10	rs1074039	0.02167	0.059658	ENSG00000227382.1
rs3180	Colon transverse_ENSG00000107731.8	20	0.756398	0.307	0.87281	1.92032	UNC5B	Colon tran GTEx_v6	T	C	73762673	10	rs2219837	-0.01048	0.058975	ENSG00000107731.8
rs3180	Brain caudate basal ganglia_E	8	0.398966	-0.660	0.872983	4.12638	P4HA1	Brain caud GTEx_v6	T	C	73858549	10	rs1668156	0.012336	0.058841	ENSG00000122884.8
rs3180	Esophagus muscularis_ENSG0	20	0.836852	0.283	0.873546	1.776899	CDH23	Esophagus GTEx_v6	T	C	73762673	10	rs2219837	-0.00964	0.058643	ENSG00000107736.15
rs3180	Stomach_ENSG00000138286.10	1	NA	-0.683	0.875416	4.355316	FAM149B1	Stomach GTEx_v6	C	G	74046191	10	rs1074039	-0.0114	0.057735	ENSG00000138286.10
rs7814941	Brain putamen basal ganglia_	18	0.744201	-0.586	0.875652	3.743458	RP11-473C	Brain puta GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.02601	0.057421	ENSG00000253720.1
rs3180	Brain frontal cortex_BA9_ENSG	1	NA	-0.788	0.876176	5.054246	MRPS16	Brain front GTEx_v6	C	G	74046191	10	rs1074039	-0.01315	0.057252	ENSG00000182180.9
rs3180	Whole blood_ENSG00000138315.8	20	0.356434	0.337	0.8763	2.162688	OIT3	Whole blo GTEx_v6	T	C	73762673	10	rs2219837	-0.01148	0.05731	ENSG00000138315.8
rs3180	Pancreas_ENSG00000227540.	1	NA	0.990	0.87666	6.377428	RP11-152N	Pancreas GTEx_v6	C	G	74046191	10	rs1074039	0.01653	0.057096	ENSG00000227540.1
rs3180	Esophagus gastroesophageal j	1	NA	-1.395	0.877362	9.039054	EIF4A2P2	Esophagus GTEx_v6	C	G	74046191	10	rs1074039	-0.02329	0.056739	ENSG00000227382.1
rs3180	Prostate_ENSG00000122884.8	8	0.704855	0.873	0.877534	5.667911	P4HA1	Prostate GTEx_v6	T	C	73858549	10	rs1668156	-0.01633	0.05655	ENSG00000122884.8
rs3180	Uterus_ENSG00000166228.4	2	NA	-0.976	0.87794	6.357189	PCBD1	Uterus GTEx_v6	C	T	73646408	10	rs1437267	-0.02138	0.056278	ENSG00000166228.4
rs3180	Brain putamen basal ganglia_	1	NA	-0.747	0.878068	4.872059	ECD	Brain puta GTEx_v6	C	G	74046191	10	rs1074039	-0.01248	0.05628	ENSG00000122882.6
rs3180	Artery tibial_ENSG00000166321.9	6	0.194127	-0.583	0.878259	3.805367	NUDT13	Artery tibi GTEx_v6	G	A	738883196	10	rs1245578	0.010842	0.056361	ENSG00000166321.9
rs3180	Brain cerebellar hemisphere_	8	0.847332	-0.684	0.880241	4.542789	P4HA1	Brain cereb GTEx_v6	T	C	73858549	10	rs1668156	0.012799	0.055219	ENSG00000122884.8
rs3180	Pituitary_ENSG00000272599.1	5	0.797296	-1.308	0.880809	8.724168	RP11-152N	Pituitary GTEx_v6	C	T	73899093	10	rs1245515	0.024331	0.054932	ENSG00000272599.1
rs3180	Stomach_ENSG00000168209.4	20	0.195351	0.339	0.881327	2.271197	DDIT4	Stomach GTEx_v6	T	C	73762673	10	rs2219837	-0.01156	0.054765	ENSG00000168209.4
rs3180	Spleen_ENSG00000107742.8	20	0.416286	-0.499	0.882522	3.376538	SPOCK2	Spleen GTEx_v6	T	C	73762673	10	rs2219837	0.017015	0.054069	ENSG00000107742.8
rs3180	Small intestine terminal ileum	20	0.330672	-0.526	0.882569	3.563207	CDH23	Small intest GTEx_v6	T	C	73762673	10	rs2219837	0.017948	0.053998	ENSG00000107736.15
rs3180	Pituitary_ENSG00000122884.8	8	0.440741	0.923	0.882859	6.267425	P4HA1	Pituitary GTEx_v6	T	C	73858549	10	rs1668156	-0.01727	0.053925	ENSG00000122884.8
rs7814941	Brain putamen basal ganglia_	18	0.457841	-0.559	0.883193	3.80651	RP11-473C	Brain puta GTEx_v6	A	G	1.31E+08	8	rs1095648	-0.02483	0.053712	ENSG00000254317.1

rs3180	Brain cerebellum_ENSG00000	16	0.47243	0.495	0.884532	3.411348	RPL17P50	Brain cere	GTEEx_v6	A	G	73820622	10 rs3180	-0.0165	0.053122	ENSG00000213700.3
rs3180	Skin not sun exposed suprapu	16	0.24185	0.300	0.885129	2.075093	RPL17P50	Skin not su	GTEEx_v6	A	G	73820622	10 rs3180	-0.00998	0.052916	ENSG00000213700.3
rs3180	Small intestine terminal ileum	1	NA	-1.447	0.88568	10.0619	RP11-1521	Small intes	GTEEx_v6	C	G	74046191	10 rs1074039	-0.02416	0.052517	ENSG00000227540.1
rs3180	Pituitary_ENSG00000166228.	2	NA	-0.840	0.88662	5.891863	PCBD1	Pituitary	GTEEx_v6	C	T	73646408	10 rs1437267	-0.0184	0.05209	ENSG00000166228.4
rs3180	Pituitary_ENSG00000122863.	20	0.241084	0.402	0.886671	2.82363	CHST3	Pituitary	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01372	0.052033	ENSG00000122863.5
rs3180	Prostate_ENSG00000237512.	20	0.463777	0.533	0.886672	3.739963	UNC5B-AS	Prostate	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01818	0.052036	ENSG00000237512.2
rs3180	Cells EBV-transformed lympho	20	0.366613	0.554	0.887394	3.915561	PSAP	Cells EBV-t	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01891	0.051744	ENSG00000197746.9
rs3180	Cells EBV-transformed lympho	20	0.155849	0.348	0.888471	2.483657	ANAPC16	Cells EBV-t	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01188	0.051218	ENSG00000166295.4
rs3180	Muscle skeletal_ENSG000001	20	0.096982	-0.199	0.889989	1.438859	SLC29A3	Muscle ske	GTEEx_v6	T	C	73762673	10 rs2219837	0.006787	0.050584	ENSG00000198246.7
rs3180	Stomach_ENSG00000213551.	1	NA	-0.579	0.890508	4.207695	DNAJC9	Stomach	GTEEx_v6	C	G	74046191	10 rs1074039	-0.00967	0.050306	ENSG00000213551.4
rs3180	Breast mammary tissue_ENSG	1	NA	0.691	0.890512	5.016706	RP11-1521	Breast mai	GTEEx_v6	C	G	74046191	10 rs1074039	0.011533	0.050313	ENSG00000227540.1
rs3180	Liver_ENSG00000107745.12	20	0.252344	0.297	0.890995	2.166218	MICU1	Liver	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01012	0.049957	ENSG00000107745.12
rs3180	Muscle skeletal_ENSG000001	1	NA	0.384	0.891109	2.801684	FAM149B1	Muscle ske	GTEEx_v6	C	G	74046191	10 rs1074039	0.006405	0.050071	ENSG00000138286.10
rs3180	Brain cerebellar hemisphere_	20	0.111965	0.665	0.891882	4.892927	RP11-354E	Brain cere	GTEEx_v6	T	C	73762673	10 rs2219837	-0.02268	0.049504	ENSG00000272627.1
rs3180	Artery tibial_ENSG000001662	2	NA	0.312	0.892559	2.312729	PCBD1	Artery tibi	GTEEx_v6	C	T	73646408	10 rs1437267	0.006841	0.049346	ENSG00000166228.4
rs3180	Colon transverse_ENSG00000	20	0.497538	0.473	0.892743	3.508049	UNC5B-AS	Colon tran	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01613	0.049184	ENSG00000237512.2
rs3180	Artery coronary_ENSG0000002	20	0.338606	0.330	0.893674	2.469359	UNC5B-AS	Artery coro	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01125	0.048695	ENSG00000237512.2
rs3180	Muscle skeletal_ENSG000002	5	0.121484	0.592	0.894018	4.440345	SNORA11	Muscle ske	GTEEx_v6	C	T	73899093	10 rs1245515	-0.011	0.048643	ENSG00000221164.1
rs3180	Cells EBV-transformed lympho	8	0.091243	0.317	0.894231	2.384062	P4HA1	Cells EBV-t	GTEEx_v6	T	C	73858549	10 rs1668156	-0.00593	0.048439	ENSG00000122884.8
rs12310519	Artery tibial_ENSG000002558	11	0.655067	0.193	0.894995	1.465038	RP11-444C	Artery tibi	GTEEx_v6	C	T	23982559	12 rs9804988	-0.0112	0.048133	ENSG00000255864.1
rs7814941	Heart atrial appendage_ENSG	19	0.50396	0.187	0.895228	1.418507	FAM49B	Heart atria	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.008294	0.047968	ENSG00000153310.14
rs7814941	Adrenal gland_ENSG0000025	19	0.7332	-0.363	0.895769	2.768635	RP11-473C	Adrenal gl	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.0161	0.047688	ENSG00000254317.1
rs3180	Pancreas_ENSG00000122882.	1	NA	-0.762	0.896728	5.871381	ECD	Pancreas	GTEEx_v6	C	G	74046191	10 rs1074039	-0.01273	0.047264	ENSG00000122882.6
rs3180	Testis_ENSG00000227540.1	1	NA	-0.549	0.898147	4.289606	RP11-1521	Testis	GTEEx_v6	C	G	74046191	10 rs1074039	-0.00917	0.046586	ENSG00000227540.1
rs3180	Brain hypothalamus_ENSG00	20	0.124154	0.722	0.899397	5.708713	MICU1	Brain hypc	GTEEx_v6	T	C	73762673	10 rs2219837	-0.02461	0.045849	ENSG00000156026.10
rs7814941	Brain cerebellum_ENSG00000	18	0.242215	0.406	0.899455	3.211932	RP11-473C	Brain cere	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.018019	0.045876	ENSG00000254317.1
rs3180	Brain cortex_ENSG000001077	20	0.904544	-0.301	0.900649	2.410256	UNC5B	Brain corte	GTEEx_v6	T	C	73762673	10 rs2219837	0.010261	0.045289	ENSG00000107731.8
rs3180	Thyroid_ENSG00000107745.1	20	0.189296	-0.187	0.900661	1.497314	MICU1	Thyroid	GTEEx_v6	T	C	73762673	10 rs2219837	0.006373	0.045395	ENSG00000107745.12
rs3180	Skin not sun exposed suprapu	20	0.19962	-0.219	0.900842	1.760168	MICU	Skin not su	GTEEx_v6	T	C	73762673	10 rs2219837	0.007479	0.045283	ENSG00000156026.10
rs7814941	Spleen_ENSG00000254317.1	17	0.840545	0.395	0.900999	3.17518	RP11-473C	Spleen	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.017538	0.045102	ENSG00000254317.1
rs3180	Small intestine terminal ileum	20	0.452035	0.503	0.901358	4.059706	PSAP	Small intest	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01716	0.044892	ENSG00000197746.9
rs3180	Brain cerebellum_ENSG00000	20	0.431894	0.427	0.901843	3.45896	OIT3	Brain cere	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01455	0.044729	ENSG00000138315.8
rs3180	Brain cortex_ENSG000002725	5	0.186849	1.174	0.902361	9.572056	RP11-1521	Brain cort	GTEEx_v6	C	T	73899093	10 rs1245515	-0.02184	0.044483	ENSG00000272599.1
rs7814941	Colon transverse_ENSG00000	19	0.421231	-0.294	0.90424	2.442634	GSDMC	Colon tran	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.01305	0.043634	ENSG00000147697.4
rs3180	Brain hypothalamus_ENSG00	20	0.394723	-0.352	0.905134	2.950785	UNC5B	Brain hypc	GTEEx_v6	T	C	73762673	10 rs2219837	0.011992	0.0431	ENSG00000107731.8
rs3180	Adrenal gland_ENSG0000010	20	0.239409	0.262	0.905776	2.212487	MICU1	Adrenal gl	GTEEx_v6	T	C	73762673	10 rs2219837	-0.00893	0.042876	ENSG00000107745.12
rs12310519	Brain caudate basal ganglia_E	11	0.592918	-0.408	0.906671	3.481127	RP11-444C	Brain caud	GTEEx_v6	C	T	23982559	12 rs9804988	0.02363	0.04241	ENSG00000255864.1
rs3180	Prostate_ENSG00000122882.	1	NA	-0.632	0.907383	5.433027	ECD	Prostate	GTEEx_v6	C	G	74046191	10 rs1074039	-0.01056	0.042067	ENSG00000122882.6
rs7814941	Brain hippocampus_ENSG00	17	0.776894	0.267	0.908047	2.308317	ASAP1	Brain hipp	GTEEx_v6	A	G	1.31E+08	8 rs1095648	0.011838	0.041709	ENSG00000153317.10
rs3180	Skin sun exposed lower leg_EI	16	0.51421	0.134	0.908633	1.166977	RPL17P50	Skin sun e	GTEEx_v6	A	G	73820622	10 rs3180	-0.00446	0.041575	ENSG00000213700.3
rs3180	Esophagus muscularis_ENSG0	6	0.606544	0.481	0.908838	4.201604	NUDT13	Esophagus	GTEEx_v6	G	A	73883196	10 rs1245578	-0.00895	0.041471	ENSG00000166321.9
rs3180	Adrenal gland_ENSG0000016	6	0.073063	0.635	0.911427	5.70832	NUDT13	Adrenal gl	GTEEx_v6	G	A	73883196	10 rs1245578	-0.01181	0.040193	ENSG00000166321.9
rs3180	Heart atrial appendage_ENSG	1	NA	0.294	0.911446	2.647612	MRPS16	Heart atria	GTEEx_v6	C	G	74046191	10 rs1074039	0.004917	0.040205	ENSG00000182180.9
rs12310519	Pituitary_ENSG00000255864.	11	0.010109	-0.389	0.913086	3.568359	RP11-444C	Pituitary	GTEEx_v6	C	T	23982559	12 rs9804988	0.022551	0.039332	ENSG00000255864.1
rs3180	Brain cerebellum_ENSG00000	20	0.02823	0.435	0.91354	4.007291	UNC5B	Brain cere	GTEEx_v6	T	C	73762673	10 rs2219837	-0.01484	0.039195	ENSG00000107731.8
rs3180	Brain hippocampus_ENSG000	1	NA	-0.789	0.913627	7.27174	DNAJC9-A	Brain hipp	GTEEx_v6	C	G	74046191	10 rs1074039	-0.01317	0.039078	ENSG00000236756.4
rs3180	Adipose subcutaneous_ENSG0	20	0.00847	0.160	0.914493	1.493582	ASCC1	Adipose su	GTEEx_v6	T	C	73762673	10 rs2219837	-0.00547	0.038784	ENSG00000138303.13
rs3180	Pancreas_ENSG00000198246.	20	0.388586	-0.220	0.914512	2.052543	SLC29A3	Pancreas	GTEEx_v6	T	C	73762673	10 rs2219837	0.007514	0.038724	ENSG00000198246.7
rs7814941	Stomach_ENSG00000153317.	20	0.635196	-0.156	0.915514	1.468091	ASAP1	Stomach	GTEEx_v6	A	G	1.31E+08	8 rs1095648	-0.00692	0.038263	ENSG00000153317.10
rs3180	Ovary_ENSG00000227382.1	1	NA	1.148	0.915587	10.83162	EIF4A2P2	Ovary	GTEEx_v6	C	G	74046191	10 rs1074039	0.019173	0.038163	ENSG00000227382.1

rs7814941	Breast mammary tissue_ENSG	20	0.090475	-0.204	0.91581	1.932282	RP11-473C	Breast mai	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.00907	0.038129	ENSG00000254317.1
rs3180	Testis_ENSG00000138303.13	20	0.044764	-0.186	0.917547	1.798706	ASCC1	Testis	GTE _x _v6	T	C	73762673	10	rs2219837	0.00635	0.037295	ENSG00000138303.13
rs3180	Skin not sun exposed suprapu	1	NA	0.686	0.917771	6.648267	EIF4A2P2	Skin not su	GTE _x _v6	C	G	74046191	10	rs1074039	0.011463	0.037223	ENSG00000227382.1
rs7814941	Small intestine terminal ileum	16	0.88839	-0.437	0.918075	4.243748	GSDMC	Small intes	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.01938	0.036948	ENSG00000147697.4
rs3180	Esophagus gastroesophageal j	1	NA	0.701	0.91919	6.910614	RP11-152N	Esophagus	GTE _x _v6	C	G	74046191	10	rs1074039	0.011709	0.036521	ENSG00000227540.1
rs7814941	Testis_ENSG00000254317.1	19	0.42713	0.263	0.919226	2.589747	RP11-473C	Testis	GTE _x _v6	A	G	1.31E+08	8	rs1095648	0.011661	0.036502	ENSG00000254317.1
rs3180	Nerve tibial_ENSG0000022116	5	0.811221	-0.548	0.919527	5.424425	SNORA11	Nerve tibia	GTE _x _v6	C	T	73899093	10	rs1245515	0.010193	0.036404	ENSG00000221164.1
rs3180	Stomach_ENSG00000182180.	1	NA	-0.249	0.920624	2.49671	MRPS16	Stomach	GTE _x _v6	C	G	74046191	10	rs1074039	-0.00445	0.035863	ENSG00000182180.9
rs3180	Thyroid_ENSG00000226701.1	20	0.868173	-0.258	0.920707	2.595131	RP11-570C	Thyroid	GTE _x _v6	T	C	73762673	10	rs2219837	0.008809	0.035842	ENSG00000226701.1
rs3180	Pituitary_ENSG00000168209.	20	0.578144	-0.472	0.921232	4.77274	DDIT4	Pituitary	GTE _x _v6	T	C	73762673	10	rs2219837	0.016093	0.035491	ENSG00000168209.4
rs3180	Brain hypothalamus_ENSG00	16	0.173824	-0.364	0.921481	3.69698	RPL17P50	Brain hypc	GTE _x _v6	A	G	73820622	10	rs3180	0.012135	0.03536	ENSG00000213700.3
rs3180	Lung_ENSG00000197746.9	20	0.952297	-0.129	0.921986	1.318362	PSAP	Lung	GTE _x _v6	T	C	73762673	10	rs2219837	0.004403	0.03524	ENSG00000197746.9
rs3180	Colon sigmoid_ENSG0000010	20	0.4971	-0.323	0.922842	3.329824	UNC5B	Colon sigm	GTE _x _v6	T	C	73762673	10	rs2219837	0.010998	0.034787	ENSG00000107731.8
rs3180	Artery coronary_ENSG000001	20	0.719929	-0.182	0.922978	1.878199	MCU	Artery cori	GTE _x _v6	T	C	73762673	10	rs2219837	0.006192	0.034717	ENSG00000156026.10
rs3180	Prostate_ENSG00000197746.9	20	0.513314	0.285	0.923633	2.976705	PSAP	Prostate	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00973	0.034368	ENSG00000197746.9
rs3180	Pituitary_ENSG00000107745.	20	0.263038	0.335	0.924604	3.538626	MICU1	Pituitary	GTE _x _v6	T	C	73762673	10	rs2219837	-0.01142	0.033911	ENSG00000107745.12
rs3180	Cells EBV-transformed lympho	1	NA	0.909	0.924854	9.636658	EIF4A2P2	Cells EBV-t	GTE _x _v6	C	G	74046191	10	rs1074039	0.015179	0.033845	ENSG00000227382.1
rs3180	Ovary_ENSG00000215086.2	20	0.380697	-0.473	0.924885	5.016765	NPM1P24	Ovary	GTE _x _v6	T	C	73762673	10	rs2219837	0.016129	0.033777	ENSG00000215086.2
rs3180	Artery coronary_ENSG000001	20	0.027823	-0.212	0.926336	2.295654	UNC5B	Artery cori	GTE _x _v6	T	C	73762673	10	rs2219837	0.007238	0.033144	ENSG00000107731.8
rs3180	Cells EBV-transformed lympho	5	0.652177	0.634	0.926737	6.890865	SNORA11	Cells EBV-t	GTE _x _v6	C	T	73899093	10	rs1245515	-0.01179	0.03296	ENSG00000221164.1
rs3180	Esophagus gastroesophageal j	20	0.26126	-0.202	0.927774	2.224335	SLC29A3	Esophagus	GTE _x _v6	T	C	73762673	10	rs2219837	0.006875	0.03248	ENSG00000198246.7
rs3180	Skin sun exposed lower leg_EI	20	0.006157	-0.089	0.928801	0.994337	DNAJB12	Skin sun e	GTE _x _v6	T	C	73762673	10	rs2219837	0.00303	0.032048	ENSG00000148719.10
rs7814941	Ovary_ENSG00000153317.10	17	0.878076	0.220	0.930096	2.502501	ASAP1	Ovary	GTE _x _v6	A	G	1.31E+08	8	rs1095648	0.009747	0.031346	ENSG00000153317.10
rs3180	Whole blood_ENSG000002140	20	0.073607	0.086	0.930233	0.980095	C10orf105	Whole blo	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00293	0.031383	ENSG00000214688.4
rs3180	Spleen_ENSG00000107738.15	20	0.683842	0.184	0.930466	2.113835	C10orf54	Spleen	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00629	0.03118	ENSG00000107738.15
rs3180	Testis_ENSG00000230526.1	20	0.887059	-0.316	0.930701	3.638818	RP11-472C	Testis	GTE _x _v6	T	C	73762673	10	rs2219837	0.010789	0.031121	ENSG00000230526.1
rs3180	Lung_ENSG00000236756.4	1	NA	-0.300	0.932008	3.514123	DNAJC9-A	Lung	GTE _x _v6	C	G	74046191	10	rs1074039	-0.00501	0.030557	ENSG00000236756.4
rs3180	Spleen_ENSG00000272627.1	20	0.430042	-0.437	0.932153	5.135722	RP11-354E	Spleen	GTE _x _v6	T	C	73762673	10	rs2219837	0.01491	0.030397	ENSG00000272627.1
rs3180	Skin sun exposed lower leg_EI	1	NA	0.452	0.932574	5.346069	EIF4A2P2	Skin sun e	GTE _x _v6	C	G	74046191	10	rs1074039	0.007554	0.030297	ENSG00000227382.1
rs3180	Thyroid_ENSG00000182180.9	1	NA	0.161	0.933426	1.921493	MRPS16	Thyroid	GTE _x _v6	C	G	74046191	10	rs1074039	0.002681	0.029897	ENSG00000182180.9
rs3180	Cells transformed fibroblasts_	2	NA	0.239	0.933483	2.857996	PCBD1	Cells trans	GTE _x _v6	C	T	73646408	10	rs1437267	0.005224	0.029868	ENSG00000166228.4
rs3180	Whole blood_ENSG00000182	1	NA	0.200	0.933631	2.399596	MRPS16	Whole blo	GTE _x _v6	C	G	74046191	10	rs1074039	0.003337	0.029808	ENSG00000182180.9
rs3180	Vagina_ENSG00000215086.2	20	0.552325	-0.460	0.934156	5.573384	NPM1P24	Vagina	GTE _x _v6	T	C	73762673	10	rs2219837	0.015702	0.02945	ENSG00000215086.2
rs3180	Esophagus gastroesophageal j	1	NA	0.521	0.93417	6.305342	ECD	Esophagus	GTE _x _v6	C	G	74046191	10	rs1074039	0.008698	0.02951	ENSG00000122882.6
rs3180	Adipose visceral omentum_EI	20	0.330618	0.119	0.934512	1.443696	PSAP	Adipose vi	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00405	0.029366	ENSG00000197746.9
rs3180	Brain anterior cingulate cortex	20	0.444628	-0.357	0.935103	4.380212	DDIT4	Brain ante	GTE _x _v6	T	C	73762673	10	rs2219837	0.012162	0.028992	ENSG00000168209.4
rs3180	Adipose subcutaneous_ENSG	5	0.575129	-0.327	0.935674	4.053148	RP11-152N	Adipose su	GTE _x _v6	C	T	73899093	10	rs1245515	0.006085	0.028853	ENSG00000272599.1
rs3180	Brain cerebellar hemisphere_	1	NA	0.589	0.936291	7.366781	FAM149B1	Brain cere	GTE _x _v6	C	G	74046191	10	rs1074039	0.009834	0.028487	ENSG00000138286.10
rs3180	Adipose visceral omentum_EI	20	0.7612	-0.250	0.936491	3.140734	OIT3	Adipose vi	GTE _x _v6	T	C	73762673	10	rs2219837	0.008534	0.028448	ENSG00000138315.8
rs3180	Thyroid_ENSG00000107731.8	20	0.841491	0.139	0.936508	1.743293	UNC5B	Thyroid	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00474	0.028459	ENSG00000107731.8
rs3180	Adipose subcutaneous_ENSG	1	NA	0.209	0.936587	2.621456	FAM149B1	Adipose su	GTE _x _v6	C	G	74046191	10	rs1074039	0.003483	0.028431	ENSG00000138286.10
rs3180	Brain anterior cingulate cortex	1	NA	0.357	0.936688	4.496308	DNAJC9	Brain ante	GTE _x _v6	C	G	74046191	10	rs1074039	0.005965	0.028266	ENSG00000213551.4
rs3180	Adipose visceral omentum_EI	6	0.708462	-0.330	0.937202	4.183091	NUDT13	Adipose vi	GTE _x _v6	G	A	738883196	10	rs1245578	0.00613	0.028123	ENSG00000166321.9
rs3180	Liver_ENSG00000166228.4	2	NA	-0.466	0.937353	5.930234	PCBD1	Liver	GTE _x _v6	C	T	73646408	10	rs1437267	-0.01021	0.028007	ENSG00000166228.4
rs7814941	Heart atrial appendage_ENSG	19	0.617127	-0.135	0.938392	1.744663	ASAP1	Heart atria	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.00599	0.027558	ENSG00000153317.10
rs3180	Brain frontal cortex BA9_ENS	20	0.132499	-0.392	0.939416	5.157522	RP11-354E	Brain front	GTE _x _v6	T	C	73762673	10	rs2219837	0.013367	0.027044	ENSG00000272627.1
rs3180	Stomach_ENSG00000107745.	20	0.687667	-0.133	0.939597	1.751793	MICU1	Stomach	GTE _x _v6	T	C	73762673	10	rs2219837	0.004527	0.027008	ENSG00000107745.12
rs3180	Colon sigmoid_ENSG0000013	20	0.014126	0.126	0.941189	1.707193	ASCC1	Colon sigm	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00429	0.026258	ENSG00000138303.13
rs3180	Esophagus mucosa_ENSG000	1	NA	0.284	0.941693	3.887016	RP11-152N	Esophagus	GTE _x _v6	C	G	74046191	10	rs1074039	0.004748	0.026064	ENSG00000227540.1
rs3180	Breast mammary tissue_ENSG	20	0.559143	-0.122	0.942443	1.69251	MCU	Breast mai	GTE _x _v6	T	C	73762673	10	rs2219837	0.004167	0.025701	ENSG00000156026.10

rs3180	Uterus_ENSG00000107731.8	20	0.126409	0.270	0.943286	3.797882	UNC5B	Uterus	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00921	0.025224	ENSG00000107731.8
rs3180	Artery tibial_ENSG000002150	20	0.300768	-0.184	0.943626	2.599213	NPM1P24	Artery tibi	GTE _x _v6	T	C	73762673	10	rs2219837	0.006268	0.025175	ENSG00000215086.2
rs7814941	Artery aorta_ENSG000002543	20	0.747514	0.149	0.944356	2.140568	RP11-473C	Artery aor	GTE _x _v6	A	G	1.31E+08	8	rs1095648	0.006634	0.024825	ENSG00000254317.1
rs3180	Colon transverse_ENSG00000	6	0.228285	-0.272	0.944428	3.900153	NUDT13	Colon tran	GTE _x _v6	G	A	73883196	10	rs1245578	0.005057	0.024787	ENSG00000166321.9
rs3180	Brain cortex_ENSG000002135	1	NA	0.363	0.944591	5.219286	DNAJC9	Brain cort	GTE _x _v6	C	G	74046191	10	rs1074039	0.006058	0.024675	ENSG00000213551.4
rs3180	Small intestine terminal ileum	1	NA	-0.545	0.94555	7.984544	ECD	Small intes	GTE _x _v6	C	G	74046191	10	rs1074039	-0.00911	0.024207	ENSG00000122882.6
rs7814941	Skin sun exposed lower leg_EI	20	0.282637	-0.082	0.946256	1.21896	ASAP1	Skin sun e	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.00365	0.023968	ENSG00000153317.10
rs3180	Pancreas_ENSG00000213700.	16	0.514099	-0.155	0.947119	2.338801	RPL17P50	Pancreas	GTE _x _v6	A	G	73820622	10	rs3180	0.005166	0.023542	ENSG00000213700.3
rs3180	Ovary_ENSG00000272627.1	20	0.822258	-0.329	0.948137	5.051511	RP11-354E	Ovary	GTE _x _v6	T	C	73762673	10	rs2219837	0.011205	0.023037	ENSG00000272627.1
rs3180	Artery coronary_ENSG000001	20	0.069237	-0.160	0.948959	2.493296	ASCC1	Artery coro	GTE _x _v6	T	C	73762673	10	rs2219837	0.005443	0.022693	ENSG00000138303.13
rs3180	Small intestine terminal ileum	20	0.828541	0.363	0.949251	5.706749	UNC5B-AS	Small intes	GTE _x _v6	T	C	73762673	10	rs2219837	-0.01239	0.022515	ENSG00000237512.2
rs3180	Vagina_ENSG00000107736.15	20	0.277868	-0.193	0.950183	3.091913	CDH23	Vagina	GTE _x _v6	T	C	73762673	10	rs2219837	0.006587	0.022095	ENSG00000107736.15
rs3180	Spleen_ENSG00000156026.10	20	0.899255	0.250	0.950623	4.040746	MCU	Spleen	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00853	0.021908	ENSG00000156026.10
rs3180	Ovary_ENSG00000226701.1	20	0.209761	0.347	0.951247	5.676407	RP11-570C	Ovary	GTE _x _v6	T	C	73762673	10	rs2219837	-0.01183	0.021621	ENSG00000226701.1
rs3180	Stomach_ENSG00000107736.	20	0.167041	-0.108	0.951814	1.784161	CDH23	Stomach	GTE _x _v6	T	C	73762673	10	rs2219837	0.003677	0.021407	ENSG00000107736.15
rs3180	Pancreas_ENSG00000166228.	2	NA	0.310	0.952321	5.183322	PCBD1	Pancreas	GTE _x _v6	C	T	73646408	10	rs1437267	0.006787	0.021171	ENSG00000166228.4
rs3180	Testis_ENSG00000197746.9	20	0.33001	-0.064	0.952796	1.088972	PSAP	Testis	GTE _x _v6	T	C	73762673	10	rs2219837	0.002198	0.020957	ENSG00000197746.9
rs12310519	Skin sun exposed lower leg_EI	11	0.142839	0.085	0.953522	1.464399	RP11-444C	Skin sun e	GTE _x _v6	C	T	23982559	12	rs9804988	-0.00494	0.020649	ENSG00000255864.1
rs3180	Adipose visceral omentum_EI	20	0.51388	0.132	0.953596	2.261164	DDIT4	Adipose vi	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00449	0.020601	ENSG00000168209.4
rs12310519	Brain hypothalamus_ENSG000	11	0.490469	-0.137	0.954369	2.391335	SOX5	Brain hypc	GTE _x _v6	C	T	23982559	12	rs9804988	0.007923	0.020196	ENSG00000134532.11
rs3180	Skin not sun exposed suprapu	8	0.376796	-0.160	0.954779	2.825	P4HA1	Skin not su	GTE _x _v6	T	C	73858549	10	rs1668156	0.002996	0.020067	ENSG00000122884.8
rs3180	Brain putamen basal ganglia_	8	0.711746	-0.432	0.955264	7.694624	RP11-344N	Brain puta	GTE _x _v6	T	C	73865131	10	rs1100017	0.008029	0.019794	ENSG00000272630.1
rs12310519	Esophagus gastroesophageal	11	0.013928	0.147	0.955643	2.646243	RP11-444C	Esophagus	GTE _x _v6	C	T	23982559	12	rs9804988	-0.00852	0.019657	ENSG00000255864.1
rs3180	Heart left ventricle_ENSG000	20	0.519163	0.128	0.956275	2.336143	C10orf54	Heart left \	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00437	0.019385	ENSG00000107738.15
rs3180	Heart left ventricle_ENSG000	2	NA	0.160	0.956285	2.92435	PCBD1	Heart left \	GTE _x _v6	C	T	73646408	10	rs1437267	0.003511	0.019382	ENSG00000166228.4
rs3180	Breast mammary tissue_ENSC	20	0.969519	-0.169	0.956737	3.118189	C10orf105	Breast mai	GTE _x _v6	T	C	73762673	10	rs2219837	0.005768	0.019174	ENSG00000214688.4
rs3180	Liver_ENSG00000214688.4	20	0.599953	-0.270	0.957291	5.03314	C10orf105	Liver	GTE _x _v6	T	C	73762673	10	rs2219837	0.009191	0.018892	ENSG00000214688.4
rs3180	Skin not sun exposed suprapu	20	0.398597	-0.090	0.957443	1.685698	MICU1	Skin not su	GTE _x _v6	T	C	73762673	10	rs2219837	0.003067	0.018857	ENSG00000107745.12
rs12310519	Esophagus mucosa_ENSG000	11	0.571392	-0.086	0.958012	1.634907	SOX5	Esophagus	GTE _x _v6	C	T	23982559	12	rs9804988	0.004984	0.018606	ENSG00000134532.11
rs7814941	Small intestine terminal ileum	16	0.33134	-0.081	0.958778	1.567122	FAM49B	Small intest	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.0036	0.018198	ENSG00000153310.14
rs3180	Brain hippocampus_ENSG000	20	0.359559	-0.236	0.960104	4.723612	UNC5B-AS	Brain hipp	GTE _x _v6	T	C	73762673	10	rs2219837	0.00805	0.017589	ENSG00000237512.2
rs3180	Esophagus mucosa_ENSG000	20	0.064699	0.148	0.960191	2.958903	NPM1P24	Esophagus	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00504	0.017621	ENSG00000215086.2
rs3180	Testis_ENSG00000237512.2	20	0.817758	-0.162	0.960627	3.283132	UNC5B-AS	Testis	GTE _x _v6	T	C	73762673	10	rs2219837	0.005527	0.017409	ENSG00000237512.2
rs3180	Vagina_ENSG00000166228.4	2	NA	0.313	0.96098	6.395343	PCBD1	Vagina	GTE _x _v6	C	T	73646408	10	rs1437267	0.006852	0.017212	ENSG00000166228.4
rs3180	Brain nucleus accumbens basi	20	0.026198	0.124	0.961274	2.559033	ASCC1	Brain nuck	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00424	0.017091	ENSG00000138303.13
rs7814941	Skin not sun exposed suprapu	20	0.665237	-0.056	0.962872	1.20738	FAM49B	Skin not su	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.0025	0.016406	ENSG00000153310.14
rs3180	Whole blood_ENSG000001560	20	0.229516	0.052	0.963413	1.128048	MCU	Whole blo	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00176	0.016174	ENSG00000156026.10
rs3180	Adipose visceral omentum_EI	2	NA	0.155	0.96343	3.377947	PCBD1	Adipose vi	GTE _x _v6	C	T	73646408	10	rs1437267	0.003392	0.016153	ENSG00000166228.4
rs3180	Skin sun exposed lower leg_EI	20	0.893561	0.072	0.965187	1.643226	SLC29A3	Skin sun e	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00245	0.015374	ENSG00000198246.7
rs3180	Colon sigmoid_ENSG0000014	20	0.914116	0.121	0.967709	2.981048	DNAJB12	Colon sign	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00412	0.01422	ENSG00000148719.10
rs7814941	Brain frontal cortex BA9_ENS	18	0.544883	-0.065	0.968923	1.658365	ASAP1	Brain front	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.00287	0.013661	ENSG00000153317.10
rs7814941	Artery tibial_ENSG000001533	20	0.926379	-0.039	0.96977	1.031237	ASAP1	Artery tibi	GTE _x _v6	A	G	1.31E+08	8	rs1095648	-0.00174	0.013317	ENSG00000153317.10
rs3180	Brain cerebellum_ENSG00000	20	0.372268	0.172	0.970169	4.605257	NPM1P24	Brain cere	GTE _x _v6	T	C	73762673	10	rs2219837	-0.00587	0.013112	ENSG00000215086.2
rs3180	Spleen_ENSG00000197746.9	20	0.424512	-0.111	0.970802	3.037139	PSAP	Spleen	GTE _x _v6	T	C	73762673	10	rs2219837	0.003791	0.012821	ENSG00000197746.9
rs3180	Adipose visceral omentum_EI	1	NA	-0.075	0.970819	2.06304	MRPS16	Adipose vi	GTE _x _v6	C	G	74046191	10	rs1074039	-0.00126	0.01284	ENSG00000182180.9
rs3180	Colon transverse_ENSG00000	20	0.833918	-0.038	0.972562	1.101682	MCU	Colon tran	GTE _x _v6	T	C	73762673	10	rs2219837	0.001292	0.012059	ENSG00000156026.10
rs3180	Stomach_ENSG00000107738.	20	0.74527	-0.050	0.97327	1.482099	C10orf54	Stomach	GTE _x _v6	T	C	73762673	10	rs2219837	0.001693	0.011744	ENSG00000107738.15
rs3180	Adipose visceral omentum_EI	16	0.780671	-0.057	0.973959	1.746857	RPL17P50	Adipose vi	GTE _x _v6	A	G	73820622	10	rs3180	0.001899	0.01144	ENSG00000213700.3
rs3180	Breast mammary tissue_ENSC	1	NA	-0.126	0.974625	3.950263	FAM149B1	Breast mai	GTE _x _v6	C	G	74046191	10	rs1074039	-0.0021	0.01144	ENSG00000138286.10
rs3180	Nerve tibial_ENSG0000021468	20	0.229237	-0.078	0.975187	2.498617	C10orf105	Nerve tibi	GTE _x _v6	T	C	73762673	10	rs2219837	0.00265	0.010899	ENSG00000214688.4

rs3180	Artery aorta_ENSG000002377	11	0.858666	-0.085	0.975191	2.717674	RP11-344N	Artery aor	GTEEx_v6	C	T	73832859	10	rs896074	0.002628	0.010893	ENSG00000237768.2
rs12310519	Heart atrial appendage_ENSG	11	0.804276	0.064	0.975464	2.095282	SOX5	Heart atria	GTEEx_v6	C	T	23982559	12	rs9804988	-0.00373	0.010766	ENSG00000134532.11
rs3180	Small intestine terminal ileum	20	0.526862	-0.129	0.975827	4.265642	DDIT4	Small intes	GTEEx_v6	T	C	73762673	10	rs2219837	0.004408	0.010579	ENSG00000168209.4
rs3180	Esophagus mucosa_ENSG00000221164.1	5	0.822957	-0.132	0.978425	4.889227	SNORA11	Esophagus	GTEEx_v6	C	T	73899093	10	rs1245515	0.002459	0.009461	ENSG00000221164.1
rs3180	Pituitary_ENSG00000221164.1	5	0.91486	-0.296	0.979132	11.33515	SNORA11	Pituitary	GTEEx_v6	C	T	73899093	10	rs1245515	0.005515	0.009124	ENSG00000221164.1
rs3180	Brain hypothalamus_ENSG00000221164.1	2	NA	0.115	0.979303	4.445879	PCBD1	Brain hypc	GTEEx_v6	C	T	73646408	10	rs1437267	0.002526	0.009044	ENSG00000166228.4
rs12310519	Colon sigmoid_ENSG000002511	11	0.98319	-0.091	0.980509	3.743868	RP11-444C	Colon signr	GTEEx_v6	C	T	23982559	12	rs9804988	0.005296	0.008527	ENSG00000255864.1
rs3180	Adipose visceral omentum_Endothelial	20	0.772098	0.031	0.980542	1.277342	ANAPC16	Adipose vi	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00106	0.00852	ENSG00000166295.4
rs3180	Ovary_ENSG00000107731.8	20	0.551629	-0.075	0.980903	3.144271	UNC5B	Ovary	GTEEx_v6	T	C	73762673	10	rs2219837	0.002566	0.008341	ENSG00000107731.8
rs3180	Pituitary_ENSG00000272988.1	20	0.739364	-0.131	0.982214	5.874634	RP11-150C	Pituitary	GTEEx_v6	T	C	73762673	10	rs2219837	0.004466	0.007764	ENSG00000272988.1
rs3180	Heart atrial appendage_ENSG	20	0.871122	-0.047	0.982251	2.095864	MCU	Heart atria	GTEEx_v6	T	C	73762673	10	rs2219837	0.00159	0.007761	ENSG00000156026.10
rs3180	Artery tibial_ENSG00000107731.8	20	0.585445	0.043	0.982728	2.005233	CDH23	Artery tibi	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00148	0.007559	ENSG00000107736.15
rs3180	Small intestine terminal ileum	20	0.487566	-0.069	0.982778	3.211218	ASCC1	Small intes	GTEEx_v6	T	C	73762673	10	rs2219837	0.002364	0.00751	ENSG00000138303.13
rs3180	Muscle skeletal_ENSG00000107731.8	20	0.777048	0.027	0.982801	1.234449	MICU1	Muscle ske	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00091	0.007528	ENSG00000107745.12
rs3180	Brain cerebellum_ENSG000000	20	0.993755	0.077	0.982826	3.599548	PSAP	Brain cereb	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00264	0.0075	ENSG00000197746.9
rs12310519	Brain anterior cingulate cortex	11	0.629556	0.036	0.983588	1.726555	SOX5	Brain ante	GTEEx_v6	C	T	23982559	12	rs9804988	-0.00206	0.007151	ENSG00000134532.11
rs3180	Cells EBV-transformed lymphocytes	20	0.112704	-0.049	0.984373	2.524799	DDIT4	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	0.001686	0.006822	ENSG00000168209.4
rs3180	Cells EBV-transformed lymphocytes	20	0.098455	-0.038	0.984686	1.979313	DNAJB12	Cells EBV-t	GTEEx_v6	T	C	73762673	10	rs2219837	0.001296	0.006684	ENSG00000148719.10
rs3180	Cells transformed fibroblasts	20	0.520964	0.043	0.985288	2.353052	C10orf105	Cells trans	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00148	0.00643	ENSG00000214688.4
rs3180	Colon sigmoid_ENSG00000272988.1	5	0.392551	-0.116	0.985902	6.586843	RP11-152C	Colon signr	GTEEx_v6	C	T	73899093	10	rs1245515	0.002165	0.006151	ENSG00000272599.1
rs3180	Small intestine terminal ileum	1	NA	-0.144	0.985981	8.192628	FAM149B1	Small intes	GTEEx_v6	C	G	74046191	10	rs1074039	-0.0024	0.006104	ENSG00000138286.10
rs3180	Pituitary_ENSG00000272630.1	8	0.361945	-0.145	0.986155	8.378632	RP11-344N	Pituitary	GTEEx_v6	T	C	73865131	10	rs1100017	0.002704	0.006031	ENSG00000272630.1
rs3180	Brain cerebellar hemisphere	20	0.013599	-0.069	0.986488	4.051977	MCU	Brain cereb	GTEEx_v6	T	C	73762673	10	rs2219837	0.00234	0.005886	ENSG00000156026.10
rs3180	Brain caudate basal ganglia_Endothelial	20	0.098991	-0.058	0.988438	3.970566	DNAJB12	Brain caud	GTEEx_v6	T	C	73762673	10	rs2219837	0.001962	0.005034	ENSG00000148719.10
rs3180	Lung_ENSG00000138286.10	1	NA	0.030	0.990117	2.381735	FAM149B1	Lung	GTEEx_v6	C	G	74046191	10	rs1074039	0.000493	0.004309	ENSG00000138286.10
rs3180	Liver_ENSG00000166295.4	20	0.442608	-0.039	0.990154	3.178597	ANAPC16	Liver	GTEEx_v6	T	C	73762673	10	rs2219837	0.001338	0.004283	ENSG00000166295.4
rs3180	Uterus_ENSG00000215086.2	20	0.364761	0.075	0.99036	6.211388	NPM1P24	Uterus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00256	0.004185	ENSG00000215086.2
rs3180	Colon transverse_ENSG000000	1	NA	-0.025	0.991447	2.363078	MRPS16	Colon tran	GTEEx_v6	C	G	74046191	10	rs1074039	-0.00042	0.003723	ENSG00000182180.9
rs3180	Thyroid_ENSG00000200170.1	20	0.541217	0.026	0.991848	2.572624	Y_RNA	Thyroid	GTEEx_v6	T	C	73762673	10	rs2219837	-0.0009	0.003551	ENSG00000200170.1
rs3180	Muscle skeletal_ENSG00000107731.8	1	NA	-0.018	0.992627	1.997786	MRPS16	Muscle ske	GTEEx_v6	C	G	74046191	10	rs1074039	-0.00031	0.003211	ENSG00000182180.9
rs3180	Whole blood_ENSG00000168209.4	20	0.779358	-0.009	0.993547	1.121798	DDIT4	Whole blo	GTEEx_v6	T	C	73762673	10	rs2219837	0.000309	0.002809	ENSG00000168209.4
rs7814941	Artery tibial_ENSG000002543	20	0.97378	-0.016	0.993859	2.031087	RP11-473C	Artery tibi	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.00069	0.002672	ENSG00000254317.1
rs3180	Prostate_ENSG00000227540.1	1	NA	-0.049	0.994256	6.801513	RP11-152C	Prostate	GTEEx_v6	C	G	74046191	10	rs1074039	-0.00082	0.002493	ENSG00000227540.1
rs3180	Adipose subcutaneous_ENSG	20	0.570962	0.016	0.995047	2.626517	RP11-354E	Adipose su	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00056	0.002154	ENSG00000272627.1
rs3180	Heart atrial appendage_ENSG	16	0.057275	0.009	0.995507	1.668319	RPL17P50	Heart atria	GTEEx_v6	A	G	73820622	10	rs3180	-0.00031	0.001952	ENSG00000213700.3
rs3180	Thyroid_ENSG00000198246.7	20	0.731758	0.010	0.995509	1.806461	SLC29A3	Thyroid	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00035	0.001953	ENSG00000198246.7
rs3180	Artery coronary_ENSG0000001	20	0.915881	-0.012	0.996257	2.647707	CDH23	Artery cor	GTEEx_v6	T	C	73762673	10	rs2219837	0.000424	0.001624	ENSG00000107736.15
rs7814941	Spleen_ENSG00000153317.10	17	0.61752	-0.010	0.99721	2.843266	ASAP1	Spleen	GTEEx_v6	A	G	1.31E+08	8	rs1095648	-0.00044	0.001209	ENSG00000153317.10
rs3180	Adipose visceral omentum_Endothelial	1	NA	-0.019	0.997333	5.607224	DNAJC9-A	Adipose vi	GTEEx_v6	C	G	74046191	10	rs1074039	-0.00031	0.001158	ENSG00000236756.4
rs3180	Esophagus gastroesophageal junction	20	0.84493	0.006	0.998415	2.79178	UNC5B-AS	Esophagus	GTEEx_v6	T	C	73762673	10	rs2219837	-0.00019	0.000687	ENSG00000237512.2

Supplementary Table 2D. Results of SMR/HEIDI analysis for back pain risk factors

beta_smr	gwas_1	gwas_2	locus	n_heidi	p_heidi	p_smr	sigma_smr	snps_heidi	a1_REF	a2_REF	bp_REF	chr_REF	rsid_REF	beta_G2	p_G2
6.012613	cLBP	Height	rs7814941	19	5.58E-12	3.6E-13	0.82705	rs1095648	A	G	1.31E+08	8	rs1095648	0.26696	90.36217
0.067909	cLBP	Disc_probl	rs3180	20	0.752926	3.3E-07	0.013302	rs2219837	T	C	73762673	10	rs2219837	-0.00232	13.2342
0.049558	cLBP	Disc_probl	rs1231051	10	0.118323	3.75E-07	0.009753	rs9804988	C	T	23982559	12	rs9804988	-0.00287	9.920421
0.039815	cLBP	Disc_probl	rs7814941	19	0.501598	3.17E-05	0.00957	rs1095648	A	G	1.31E+08	8	rs1095648	0.001768	6.065886
-1.67736	cLBP	Height	rs3180	20	0.787751	4.35E-05	0.410286	rs2219837	T	C	73762673	10	rs2219837	0.057198	6.358933
Threshold SMR				0.00098											
0.80038	cLBP	Height	rs1231051	10	0.011238	0.007385	0.298764	rs9804988	C	T	23982559	12	rs9804988	-0.04634	2.334166
Suggestive threshold SMR				0.009804											
-0.66291	cLBP	BMI	rs7814941	19	0.069438	0.011758	0.263129	rs1095648	A	G	1.31E+08	8	rs1095648	-0.02943	2.110077
-0.04462	cLBP	Osteoarthr	rs3180	20	0.535684	0.019246	0.019061	rs2219837	T	C	73762673	10	rs2219837	0.001521	1.888267
0.034851	cLBP	Osteoarthr	rs1231051	10	0.36502	0.027906	0.015852	rs9804988	C	T	23982559	12	rs9804988	-0.00202	1.64643
0.604751	cLBP	BMI	rs3180	20	0.819487	0.038017	0.291492	rs2219837	T	C	73762673	10	rs2219837	-0.02062	1.52663
0.011147	cLBP	Anxiety	rs7814941	19	0.977936	0.114228	0.007057	rs1095648	A	G	1.31E+08	8	rs1095648	0.000495	0.971632
-2.72193	cLBP	B5_OPENN	rs1231051	7	0.438662	0.192424	2.088268	rs9804988	C	T	23982559	12	rs9804988	0.1576	0.728623
2.846608	cLBP	B5_CONSC	rs3180	20	0.319234	0.208798	2.264827	rs751450;rA	G	73761015	10	rs751450	-0.0965	0.696372	
0.003553	cLBP	Scoliosis	rs7814941	19	0.061906	0.24217	0.003038	rs1095648	A	G	1.31E+08	8	rs1095648	0.000158	0.625618
0.016132	cLBP	Depressior	rs7814941	19	0.930836	0.242362	0.013798	rs1095648	A	G	1.31E+08	8	rs1095648	0.000716	0.625233
3.029613	cLBP	B5_NEURC	rs7814941	12	0.504525	0.242591	2.592658	rs7833174	T	C	1.31E+08	8	rs7833174	0.133	0.625068
0.008531	cLBP	Osteoporos	rs7814941	19	0.911911	0.249336	0.007405	rs1095648	A	G	1.31E+08	8	rs1095648	0.000379	0.612397
-0.0459	cLBP	Smoking_s	rs3180	20	0.382843	0.278963	0.042399	rs2219837	T	C	73762673	10	rs2219837	0.001565	0.563694
2.80531	cLBP	B5_NEURC	rs3180	20	0.7452	0.330223	2.881183	rs751450;rA	G	73761015	10	rs751450	-0.0951	0.487582	
0.002677	cLBP	Scoliosis	rs1231051	10	0.494793	0.351887	0.002875	rs9804988	C	T	23982559	12	rs9804988	-0.00015	0.457424
-0.08212	cLBP	Happiness	rs3180	20	0.168455	0.360848	0.089867	rs2219837	T	C	73762673	10	rs2219837	0.0028	0.447731
-0.00299	cLBP	Scoliosis	rs3180	20	0.158075	0.376794	0.003383	rs2219837	T	C	73762673	10	rs2219837	0.000102	0.428431
2.468048	cLBP	B5_NEURC	rs1231051	7	0.576047	0.38158	2.820662	rs9804988	C	T	23982559	12	rs9804988	-0.1429	0.42159
-0.0055	cLBP	Anxiety	rs1231051	10	0.590862	0.40485	0.006608	rs9804988	C	T	23982559	12	rs9804988	0.000319	0.395277
-1.87392	cLBP	B5_EXTRA	rs1231051	7	0.74467	0.410223	2.275555	rs9804988	C	T	23982559	12	rs9804988	0.1085	0.389553
0.01288	cLBP	Osteoarthr	rs7814941	19	0.367226	0.425117	0.016149	rs1095648	A	G	1.31E+08	8	rs1095648	0.000572	0.373999
1.544419	cLBP	B5_OPENN	rs7814941	12	0.828391	0.425925	1.939778	rs7833174	T	C	1.31E+08	8	rs7833174	0.0678	0.373454
-1.41593	cLBP	B5_AGREE	rs3180	20	0.170018	0.445996	1.857915	rs751450;rA	G	73761015	10	rs751450	0.048	0.3534	
0.005911	cLBP	Anxiety	rs3180	20	0.721078	0.446709	0.007769	rs2219837	T	C	73762673	10	rs2219837	-0.0002	0.352646
1.209567	cLBP	B5_AGREE	rs7814941	12	0.198807	0.470764	1.677074	rs7833174	T	C	1.31E+08	8	rs7833174	0.0531	0.328827
-1.35693	cLBP	B5_OPENN	rs3180	20	0.441061	0.524086	2.129993	rs751450;rA	G	73761015	10	rs751450	0.046	0.28208	

0.00714	cLBP	Depressior	rs1231051	10	0.071954	0.583061	0.013007	rs9804988	C	T	23982559	12	rs9804988	-0.00041	0.234905
0.020483	cLBP	Smoking_s	rs7814941	19	0.627267	0.585666	0.037574	rs1095648	A	G	1.31E+08	8	rs1095648	0.000909	0.233037
0.918826	cLBP	B5_AGREE	rs1231051	7	0.251615	0.609657	1.799632	rs9804988	C	T	23982559	12	rs9804988	-0.0532	0.215525
-1.03189	cLBP	B5_EXTRA'	rs7814941	12	0.60092	0.613914	2.045395	rs7833174	T	C	1.31E+08	8	rs7833174	-0.0453	0.212327
0.034542	cLBP	EduYears2	rs1231051	11	0.098334	0.617717	0.069211	rs9804988	C	T	23982559	12	rs9804988	-0.002	0.17192
0.036085	cLBP	Happiness	rs7814941	20	0.357909	0.651281	0.079837	rs1095648	A	G	1.31E+08	8	rs1095648	0.001602	0.186598
0.032963	cLBP	Happiness	rs1231051	11	0.127484	0.664459	0.075992	rs9804988	C	T	23982559	12	rs9804988	-0.00191	0.177815
-0.09584	cLBP	Fluid_intel	rs1231051	11	0.099229	0.676512	0.229707	rs9804988	C	T	23982559	12	rs9804988	0.005549	0.169974
-0.0061	cLBP	Depressior	rs3180	20	0.381272	0.689749	0.01527	rs2219837	T	C	73762673	10	rs2219837	0.000208	0.161617
-0.79102	cLBP	B5_CONSC	rs1231051	7	0.798719	0.717783	2.188619	rs9804988	C	T	23982559	12	rs9804988	0.0458	0.144178
-0.72566	cLBP	B5_EXTRA'	rs3180	20	0.497743	0.752104	2.297381	rs751450;	A	G	73761015	10	rs751450	0.0246	0.123724
0.002074	cLBP	Osteoporo	rs1231051	10	0.028341	0.76607	0.006972	rs9804988	C	T	23982559	12	rs9804988	-0.00012	0.115817
0.066617	cLBP	Fluid_intel	rs7814941	20	0.052891	0.78227	0.241048	rs1095648	A	G	1.31E+08	8	rs1095648	0.002958	0.106717
-0.04227	cLBP	Fluid_intel	rs3180	20	0.529114	0.875298	0.269341	rs2219837	T	C	73762673	10	rs2219837	0.001441	0.057859
0.305239	cLBP	B5_CONSC	rs7814941	12	0.417095	0.879132	2.007225	rs7833174	T	C	1.31E+08	8	rs7833174	0.0134	0.055912
-0.00249	cLBP	Smoking_s	rs1231051	10	0.017016	0.944371	0.035658	rs9804988	C	T	23982559	12	rs9804988	0.000144	0.024858
-0.00035	cLBP	Osteoporo	rs3180	20	0.992326	0.965818	0.008184	rs2219837	T	C	73762673	10	rs2219837	1.2E-05	0.015104
-0.00629	cLBP	BMI	rs1231051	10	0.029477	0.978808	0.236875	rs9804988	C	T	23982559	12	rs9804988	0.000364	0.009302
0 cLBP		EduYears2	rs7814941	20		1		rs1095648	A	G	1.31E+08	8	rs1095648	0	0.03659
0 cLBP		EduYears2	rs3180	20		1		rs2219837	T	C	73762673	10	rs2219837	0	0.034939

Supplementary Table 3A: Results of univariate and COJO analyses and replication of back pain GWAS using UK Biobank data

Proxy	SNP	Gene by	Gene by	Chr	(bp)	Allele	Allele	UKBB univariate				N effectiv	Joint effects and approximate conditional analysis				Replication				Sign disc	N	Replicate	be	be	on							
								MACH	R	Frequenc	Beta		T^2 statis	T^2 GC	G	P-value	LD (r2)	EAF	BETA	SE	P-value												
rs7134574	rs12310519	SOX5		12	2.4E+07	C	T	0.99112	0.84	-0.056	0.0073	1.38E-14	59.26	57.42	3.52E-14	350000	363135	0.84	-0.056	0.0073	1.39E-14	0.000	0.84	-0.05	0.011	5.00E-05	1	157618	1	0.92984	0.99146	0.98721	TRUE
rs1865442		C8orf34		8	7E+07	C	T	0.99287	0.82	-0.052	0.0070	1.60E-13	54.44	52.75	3.79E-13	350000	366950	0.82	-0.052	0.0070	1.60E-13	0.000	0.82	-0.03	0.011	0.01052	1	157724	0	0.90428	0.98533	0.97848	TRUE
rs3180		SPOCK2	SPOCK2	10	7.4E+07	A	G	0.99764	0.44	-0.037	0.0055	7.83E-12	46.81	45.35	1.65E-11	350000	359458	0.44	-0.037	0.0055	7.86E-12	0.000	0.44	-0.02	0.008	6.59E-03	1	157731	1	0.84701	0.96657	0.95272	TRUE
rs7814941		GSDMC		8	1.3E+08	A	G	0.99849	0.80	0.046	0.00681	1.81E-11	45.17	43.76	3.71E-11	350000	358807	0.75	0.046	0.00681	1.82E-11	0.000	0.75	0.04	0.010	5.32E-05	1	157728	1	0.83151	0.96036	0.94438	TRUE
rs2672596		HTRA1		10	1.2E+08	G	A	0.99457	0.74	0.041	0.0063	4.46E-11	43.40	42.05	8.89E-11	350000	355894	0.76	0.041	0.0063	6.14E-11	0.009	0.76	0.02	0.010	0.03982	1	157735	0	0.81337	0.95248	0.93394	TRUE
rs1087024		DPYSL4		10	1.3E+08	C	T	0.99141	0.44	0.030	0.00551	3.09E-08	30.65	29.70	5.05E-08	350000	358771	0.47	0.030	0.00551	4.25E-08	0.000	0.47	0.01	0.009	0.22	1	154970	0	0.63197	0.83934	0.79312	FALSE
rs4974563		KIAA1530	SPON2	4	1138153	C	T	1.00099	0.30	-0.032	0.0059	4.39E-08	29.97	29.04	7.10E-08	350000	359866	0.34	-0.032	0.0059	4.39E-08	0.000	0.34	-0.02	0.009	0.02717	1	154970	0	0.61963	0.82941	0.78136	FALSE
rs2910576		PLK2		5	5.8E-07	A	T	0.99396	0.19	0.038	0.00691	4.71E-08	29.83	28.90	7.60E-08	350000	365547	0.20	0.038	0.00691	4.72E-08	0.000	0.20	0.02	0.010	0.1076	1	157742	0	0.61713	0.82737	0.77895	FALSE
rs7105462		NCAM1		11	1.E+08	G	A	0.99805	0.41	0.030	0.0055	4.72E-08	29.83	28.90	7.62E-08	350000	362341	0.44	0.030	0.0055	4.72E-08	0.000	0.43	0.01	0.008	0.1149	1	157752	0	0.61704	0.82729	0.77887	FALSE
rs10502966		DCC		18	5.1E+07	A	G	0.99673	0.58	-0.030	0.0065	4.94E-08	29.74	28.82	7.96E-08	350000	362262	0.60	-0.030	0.0065	4.95E-08	0.000	0.60	-0.02	0.009	9.66E-03	1	157752	0	0.61543	0.82597	0.7773	FALSE

Supplementary Table 3B. Results of univariate and COJO analyses of back pain GWAS with p-value<=1e-5.

Chr	SNP	bp	refA	freq	b	se	p	n	freq_gen	bJ	bJ_se	pJ	LD_r
10	rs2815548	27960532	G	0.245387	-0.02821	0.006329	8.28E-06	358285	0.242796	-0.02821	0.006329	8.28E-06	0
10	rs5578591	70618070	A	0.827188	0.033631	0.00722	3.19E-06	356653	0.821797	0.033898	0.00722	2.67E-06	0.005414
10	rs3180	73820622	A	0.441095	-0.03746	0.005476	7.83E-12	359458	0.440355	-0.0376	0.005476	6.59E-12	0
10	rs1209870	88074595	G	0.999529	-0.53888	0.120369	7.57E-06	389608	0.99945	-0.53747	0.120372	8.01E-06	-0.00297
10	rs1831477	88311564	T	0.995576	0.202103	0.044877	6.68E-06	299594	0.996039	0.201581	0.044878	7.07E-06	0
10	rs5351320	1.08E+08	C	0.996481	-0.20487	0.045862	7.93E-06	360308	0.997597	-0.20487	0.045863	7.93E-06	0
10	rs2672596	1.24E+08	G	0.743509	0.041222	0.006257	4.46E-11	355894	0.739296	0.040928	0.006258	6.14E-11	0.008603
10	rs1087026	1.34E+08	C	0.439941	0.030356	0.005483	3.09E-08	358771	0.435083	0.030048	0.005483	4.25E-08	0
11	rs1413514	7509386	C	0.995693	0.2031	0.043567	3.14E-06	327235	0.99535	0.2031	0.043569	3.14E-06	0
11	rs697311	29675343	G	0.625137	-0.03013	0.005617	8.09E-08	360309	0.627769	-0.03013	0.005617	8.10E-08	0
11	rs7830140	46712123	T	0.975647	0.08334	0.018142	4.36E-06	340608	0.977496	0.08334	0.018143	4.36E-06	0
11	rs1790765	67223086	C	0.998831	-0.36638	0.073727	6.72E-07	419689	0.99865	-0.36638	0.073729	6.72E-07	0
11	rs7105462	1.13E+08	G	0.405153	0.030164	0.005523	4.72E-08	362341	0.405437	0.030164	0.005523	4.72E-08	0
11	rs3453126	1.33E+08	T	0.877921	-0.03893	0.00828	2.58E-06	362484	0.883233	-0.03893	0.008281	2.58E-06	0
12	rs1242681	6580314	A	0.770614	-0.03017	0.006432	2.71E-06	362366	0.770116	-0.03017	0.006432	2.71E-06	0
12	rs1231051	23975219	C	0.836498	-0.05623	0.007304	1.38E-14	363135	0.83928	-0.05623	0.007305	1.39E-14	0
12	rs1914266	67144701	T	0.993385	-0.1572	0.034017	3.81E-06	348486	0.995183	-0.15828	0.034019	3.27E-06	-0.00718
12	rs1927280	69712342	A	0.995453	-0.18117	0.041169	1.08E-05	345416	0.997388	-0.18254	0.041171	9.27E-06	0
12	rs7302816	89950320	A	0.802764	-0.03425	0.006839	5.48E-07	357853	0.805784	-0.03425	0.006839	5.48E-07	0
12	rs9669131	1.12E+08	A	0.78887	-0.03021	0.006662	5.75E-06	358508	0.790908	-0.03021	0.006662	5.75E-06	0
12	rs7144456	1.24E+08	G	0.799317	0.032952	0.006818	1.34E-06	355387	0.806568	0.033144	0.006818	1.17E-06	-0.00589
12	rs1105814	1.26E+08	G	0.901798	0.044846	0.009301	1.42E-06	345873	0.904548	0.045109	0.009302	1.24E-06	0
13	rs1513340	49737309	A	0.998703	-0.3757	0.082142	4.79E-06	303628	0.999299	-0.3696	0.082155	6.83E-06	-0.00706
13	rs1443914	53917230	T	0.471681	0.027878	0.005436	2.92E-07	360413	0.469695	0.02614	0.005441	1.55E-06	-0.03516
13	rs1405591	54775997	G	0.990218	-0.14283	0.028103	3.73E-07	346878	0.991785	-0.138	0.028122	9.23E-07	-0.00536
13	rs6195760	59079147	T	0.781019	0.034052	0.006662	2.69E-07	354083	0.782288	0.032925	0.006623	6.64E-07	0.007277
13	rs1399175	67036110	T	0.99	-0.12618	0.028096	7.09E-06	339572	0.99289	-0.12717	0.028098	6.01E-06	0
13	rs5345542	78758771	C	0.998801	-0.36256	0.076394	2.07E-06	379701	0.998849	-0.36256	0.076396	2.08E-06	0
13	rs5652214	99172895	C	0.999668	-0.66893	0.14375	3.26E-06	386944	0.9997	-0.68035	0.143771	2.22E-06	-0.00243
13	rs1434302	1.02E+08	G	0.994327	-0.15804	0.036124	1.21E-05	360522	0.995131	-0.15985	0.036126	9.66E-06	-0.00874
13	rs7983579	1.07E+08	G	0.440522	-0.02391	0.005485	1.31E-05	357937	0.438665	-0.02452	0.005486	7.82E-06	0
14	rs7147566	30608327	G	0.722703	0.026788	0.006097	1.11E-05	357043	0.71881	0.027006	0.006099	9.51E-06	-0.01846
14	rs2383521	34124524	T	0.508627	0.02472	0.005446	5.64E-06	358838	0.51369	0.02594	0.00545	1.94E-06	0.006406
14	rs5470220	35371330	G	0.999001	-0.41784	0.09206	5.66E-06	314457	0.99965	-0.41167	0.092081	7.79E-06	-0.01008
14	rs8022156	37657148	T	0.734717	0.031798	0.006191	2.80E-07	356072	0.74019	0.032412	0.006195	1.67E-07	0.00405
14	rs1087295	42195024	T	0.691247	-0.03189	0.00586	5.27E-08	362862	0.694217	-0.032	0.005863	4.81E-08	-0.02444

14	rs6199046	42382758	A	0.997734	-0.27707	0.057612	1.52E-06	354436	0.998246	-0.29014	0.057635	4.80E-07	0
14	rs8013931	63338563	A	0.861673	0.037	0.007957	3.32E-06	352469	0.862303	0.036784	0.007957	3.79E-06	-0.00556
14	rs5362973	64295695	A	0.998929	-0.43002	0.085449	4.84E-07	340486	0.999699	-0.42516	0.085455	6.52E-07	0.007257
14	rs8015288	74060127	T	0.530118	-0.02458	0.005441	6.27E-06	360705	0.521844	-0.02439	0.005441	7.40E-06	0
14	rs1919377	88564854	C	0.996825	0.23541	0.05277	8.15E-06	301791	0.996894	0.23541	0.052771	8.16E-06	0
15	rs1593612	26687550	G	0.67285	-0.02674	0.005796	3.97E-06	362259	0.670381	-0.02674	0.005796	3.97E-06	0
15	rs1422006	71742094	C	0.988301	0.130276	0.027467	2.11E-06	307047	0.991674	0.130276	0.027468	2.11E-06	0
16	rs5549427	6027869	T	0.995278	0.221182	0.045053	9.14E-07	281871	0.996283	0.221182	0.045055	9.15E-07	0
16	rs1878071	30106247	G	0.996616	0.244372	0.054396	7.04E-06	269445	0.996983	0.244372	0.054398	7.05E-06	0
16	rs4517795	52893891	T	0.433167	0.024487	0.005473	7.67E-06	365616	0.434521	0.024487	0.005473	7.68E-06	0
16	rs2247603	71609364	G	0.840285	-0.0371	0.007361	4.64E-07	369788	0.840857	-0.03744	0.007361	3.67E-07	0.009995
16	rs7193350	76404556	C	0.892794	0.039401	0.008856	8.63E-06	358197	0.893496	0.039533	0.008857	8.07E-06	0.008827
16	rs5513363	80091491	G	0.998377	0.338495	0.075757	7.89E-06	289145	0.998599	0.336174	0.075762	9.11E-06	0.000837
16	rs918722	89415081	C	0.45404	-0.02502	0.005462	4.62E-06	363660	0.451921	-0.02504	0.005462	4.55E-06	0
17	rs1844889	38244158	T	0.989179	-0.12872	0.026508	1.20E-06	359575	0.991192	-0.12872	0.026509	1.20E-06	0
17	rs1245301	50316131	C	0.605251	-0.02559	0.005567	4.30E-06	365205	0.602816	-0.02558	0.005567	4.32E-06	0.000229
17	rs1245071	55676536	G	0.897995	-0.04061	0.008927	5.39E-06	370482	0.896922	-0.0406	0.008927	5.42E-06	0
17	rs5654232	78943589	G	0.995702	-0.18519	0.041096	6.60E-06	374191	0.997197	-0.18519	0.041097	6.61E-06	0
18	rs1404444	47575472	T	0.996324	0.224856	0.048481	3.52E-06	310207	0.996595	0.219337	0.048493	6.10E-06	-0.02296
18	rs1050296	50748499	A	0.579407	-0.02999	0.0055	4.94E-08	362262	0.587232	-0.02946	0.005501	8.52E-08	0
18	rs1434474	69526447	C	0.98648	0.114104	0.025532	7.86E-06	307130	0.988999	0.114104	0.025533	7.86E-06	0
19	rs13169	808586	C	0.862859	-0.04112	0.007823	1.47E-07	370556	0.86205	-0.04112	0.007823	1.47E-07	0
19	rs1157351	11981342	G	0.99973	-0.75566	0.157083	1.50E-06	402907	0.9998	-0.75566	0.157087	1.51E-06	0
19	rs1041404	45415713	G	0.871492	0.038824	0.008182	2.09E-06	357899	0.874221	0.039227	0.008183	1.64E-06	-0.0111
19	rs3415998	46098149	G	0.984615	0.112009	0.02382	2.57E-06	312207	0.989258	0.113193	0.023823	2.02E-06	0
1	rs7994143	6039258	C	0.984899	0.104895	0.023667	9.33E-06	321518	0.986802	0.104895	0.023667	9.33E-06	0
1	rs1158591	19722082	C	0.97215	0.076519	0.01677	5.04E-06	351784	0.97115	0.076519	0.01677	5.05E-06	0
1	rs1931695	51215875	C	0.984461	-0.109	0.022465	1.22E-06	346932	0.986677	-0.109	0.022466	1.22E-06	0
1	rs1158454	72741382	T	0.683896	-0.0277	0.005821	1.94E-06	365651	0.68775	-0.0277	0.005821	1.94E-06	0
1	rs1321104	1.16E+08	G	0.107263	0.040844	0.00873	2.89E-06	367011	0.106088	0.040716	0.00873	3.11E-06	-0.00334
1	rs3528963	1.18E+08	C	0.881519	-0.03688	0.00832	9.28E-06	370485	0.88295	-0.03676	0.00832	9.98E-06	0
1	rs1895336	1.54E+08	T	0.99894	-0.39792	0.08871	7.27E-06	321431	0.999449	-0.40273	0.088718	5.64E-06	0.012411
1	rs1126454	1.57E+08	G	0.583075	0.025323	0.005533	4.73E-06	359841	0.583503	0.025618	0.005534	3.67E-06	0
1	rs7802968	2.29E+08	G	0.99925	-0.48947	0.098963	7.58E-07	364917	0.999549	-0.48947	0.098966	7.58E-07	0
20	rs6078110	1177199	A	0.820373	0.03343	0.007105	2.54E-06	359989	0.8204	0.033353	0.007105	2.68E-06	-0.00244
20	rs6037486	3091270	T	0.891288	-0.03894	0.008659	6.90E-06	368638	0.892416	-0.03884	0.008659	7.28E-06	0
20	rs5536985	21961056	T	0.998458	-0.34718	0.076354	5.44E-06	298354	0.999247	-0.34718	0.076356	5.44E-06	0
20	rs1204765	49719603	G	0.475959	0.026346	0.005431	1.23E-06	364044	0.4766	0.026346	0.005431	1.23E-06	0
21	rs1174946	34733322	G	0.971482	0.073711	0.016632	9.34E-06	349595	0.970627	0.073711	0.016632	9.35E-06	0

21	rs6221626	46798027	C	0.996068	-0.20547	0.044317	3.55E-06	348305	0.997589	-0.20547	0.044318	3.55E-06	0
22	rs5754752	34293516	T	0.490126	-0.02419	0.005439	8.69E-06	362306	0.490578	-0.02419	0.005439	8.69E-06	0
22	rs2873599	51135595	A	0.883621	-0.04005	0.008409	1.91E-06	368335	0.8847	-0.04005	0.008409	1.91E-06	0
2	rs2564039	6029014	T	0.505036	-0.02558	0.005434	2.51E-06	362765	0.505322	-0.02558	0.005434	2.51E-06	0
2	rs1247103	63484639	C	0.794279	0.032548	0.006756	1.45E-06	359065	0.790919	0.032548	0.006756	1.45E-06	0
2	rs1841406	1.42E+08	C	0.998898	-0.3794	0.085018	8.10E-06	336548	0.999349	-0.3794	0.08502	8.10E-06	0
3	rs1882605	7573002	G	0.995747	-0.1872	0.041262	5.71E-06	371248	0.995891	-0.18686	0.041264	5.94E-06	-0.00241
3	rs3715791	10287724	C	0.999572	0.828208	0.176953	2.86E-06	199811	0.99965	0.826789	0.176963	2.98E-06	0
3	rs1857597	63367695	T	0.995576	-0.19446	0.043986	9.83E-06	314126	0.996876	-0.19446	0.043987	9.83E-06	0
3	rs5458104	1.11E+08	A	0.999598	-0.6033	0.13477	7.59E-06	366757	0.99975	-0.6033	0.134773	7.59E-06	0
3	rs6229523	1.35E+08	G	0.966563	0.069348	0.015602	8.80E-06	340236	0.967898	0.069348	0.015603	8.81E-06	0
3	rs6179469	1.59E+08	A	0.82174	-0.03204	0.007071	5.85E-06	365503	0.826318	-0.03204	0.007071	5.85E-06	0
3	rs1116934	1.72E+08	T	0.997047	-0.23688	0.052845	7.38E-06	325557	0.997991	-0.23781	0.052847	6.80E-06	-0.00405
3	rs1154267	1.8E+08	T	0.996951	-0.22429	0.050097	7.57E-06	350876	0.997892	-0.22517	0.050099	6.98E-06	0
4	rs4974563	1138153	C	0.30472	-0.03233	0.005906	4.39E-08	359866	0.306113	-0.0323	0.005906	4.52E-08	-0.00116
4	rs3021146	2958186	A	0.672133	0.025661	0.00579	9.35E-06	359970	0.678096	0.025624	0.00579	9.63E-06	0
4	rs5633083	19891513	T	0.229548	-0.02846	0.006511	1.23E-05	354677	0.224606	-0.02907	0.006512	8.06E-06	0.017977
4	rs5617742	20452307	T	0.998091	0.358347	0.074119	1.33E-06	254075	0.998745	0.360446	0.074133	1.16E-06	-0.00939
4	rs1412094	26161601	C	0.978571	-0.09473	0.019236	8.45E-07	342755	0.982797	-0.09431	0.019237	9.47E-07	0
4	rs7767247	55663513	A	0.999233	-0.43273	0.095148	5.42E-06	383311	0.9994	-0.43405	0.095151	5.07E-06	-0.00323
4	rs1507974	59476221	G	0.992347	-0.15074	0.032734	4.12E-06	326828	0.99484	-0.15119	0.032735	3.87E-06	0
4	rs1313509	1.03E+08	A	0.917266	-0.04439	0.009815	6.10E-06	363779	0.916658	-0.04439	0.009815	6.11E-06	0
4	rs1167071	1.36E+08	G	0.958796	-0.06442	0.013491	1.79E-06	369856	0.960887	-0.06459	0.013492	1.69E-06	0.006927
4	rs1863065	1.38E+08	C	0.998159	0.32915	0.073927	8.49E-06	264816	0.998697	0.329358	0.073932	8.39E-06	-0.00656
4	rs1893505	1.4E+08	A	0.989708	-0.12187	0.02712	7.00E-06	355005	0.991758	-0.12077	0.027121	8.47E-06	0
4	rs9998332	1.6E+08	C	0.383958	0.027546	0.005572	7.67E-07	362136	0.38323	0.029706	0.00559	1.07E-07	0.079768
4	rs7835452	1.6E+08	A	0.976796	-0.0733	0.017709	3.49E-05	374169	0.9764	-0.08136	0.017765	4.65E-06	0.007445
4	rs6811955	1.65E+08	C	0.569329	0.027496	0.00549	5.49E-07	359849	0.570301	0.027837	0.005491	3.98E-07	0
5	rs7718889	7200526	T	0.369834	0.027057	0.005619	1.47E-06	363644	0.370943	0.026911	0.005619	1.68E-06	-0.00547
5	rs1195068	10237159	A	0.964024	-0.06992	0.01459	1.65E-06	362423	0.966027	-0.06954	0.014591	1.88E-06	0
5	rs1403753	25108087	A	0.993118	-0.157	0.033127	2.14E-06	356745	0.993964	-0.15906	0.03313	1.58E-06	-0.01119
5	rs1921117	30876763	G	0.612324	-0.02815	0.005564	4.23E-07	364057	0.610749	-0.02847	0.005565	3.13E-07	0.000897
5	rs7733331	32828846	T	0.399615	0.02559	0.005536	3.79E-06	363954	0.403628	0.025648	0.005536	3.60E-06	0
5	rs2910576	57532748	A	0.189427	0.037711	0.006904	4.71E-08	365547	0.18982	0.03775	0.006905	4.57E-08	-0.00128
5	rs2963820	59109014	A	0.811179	0.031291	0.007005	7.94E-06	355976	0.814824	0.03134	0.007006	7.69E-06	0
5	rs2434280	79388765	A	0.487579	-0.02453	0.005433	6.32E-06	362844	0.487168	-0.02453	0.005433	6.32E-06	0
5	rs4703254	1.03E+08	C	0.318835	-0.03088	0.005843	1.26E-07	360843	0.328076	-0.03257	0.005851	2.60E-08	-0.05143
5	rs1265475	1.04E+08	C	0.862382	-0.03902	0.007872	7.17E-07	363869	0.862008	-0.03884	0.007895	8.70E-07	-0.0573
5	rs396755	1.04E+08	C	0.428864	0.027198	0.005486	7.14E-07	362945	0.425954	0.026073	0.005496	2.09E-06	0.010673

5	rs5322378	1.1E+08	C	0.999611	-0.59947	0.132025	5.61E-06	394782	0.99965	-0.60235	0.13204	5.07E-06	0
5	rs917303	1.35E+08	G	0.656141	-0.02722	0.005718	1.93E-06	362719	0.659571	-0.02722	0.005718	1.94E-06	0
5	rs7579731	1.57E+08	G	0.999425	-0.56702	0.118638	1.76E-06	330809	0.99955	-0.56613	0.118642	1.83E-06	-0.00174
5	rs1158185	1.64E+08	G	0.996813	0.270283	0.056457	1.69E-06	264245	0.998344	0.271394	0.05646	1.53E-06	-0.00633
5	rs1047597	1.71E+08	G	0.526563	0.027136	0.005444	6.22E-07	362117	0.522711	0.027277	0.005445	5.44E-07	0
6	rs5772331	25017102	T	0.996427	0.229841	0.051915	9.54E-06	275617	0.99794	0.232765	0.051924	7.37E-06	0.009008
6	rs2393649	26338538	T	0.690202	0.026951	0.005905	5.02E-06	354663	0.691422	0.026844	0.005906	5.49E-06	0.00632
6	rs1215385	32074804	T	0.896195	-0.04531	0.008816	2.75E-07	365758	0.89805	-0.04634	0.008818	1.48E-07	0.005281
6	rs1427761	33778776	T	0.997697	0.310862	0.065931	2.42E-06	264784	0.998797	0.312376	0.065935	2.16E-06	0
6	rs1319525	53777087	A	0.99428	-0.16335	0.035393	3.93E-06	371231	0.994291	-0.16335	0.035394	3.93E-06	0
6	rs1017741	81536262	T	0.522307	-0.02494	0.005438	4.51E-06	358391	0.526239	-0.02493	0.005439	4.57E-06	-0.00045
6	rs1163828	85801160	G	0.974284	0.088826	0.017486	3.78E-07	345238	0.9729	0.088791	0.017486	3.82E-07	0
6	rs265360	1.3E+08	T	0.222267	-0.03251	0.006569	7.49E-07	354515	0.220157	-0.03251	0.006569	7.50E-07	0
7	rs1025637	3690843	A	0.768236	0.028585	0.006463	9.75E-06	358931	0.771651	0.028585	0.006464	9.75E-06	0
7	rs5284185	17450561	C	0.999649	-0.68906	0.138103	6.05E-07	398942	0.9997	-0.68958	0.138107	5.94E-07	-0.00081
7	rs1921872	25820527	C	0.999403	-0.48773	0.106661	4.81E-06	393322	0.99945	-0.48816	0.106664	4.72E-06	0
7	rs2299212	86302469	A	0.36966	0.028812	0.005611	2.82E-07	363919	0.366763	0.028812	0.005611	2.82E-07	0
7	rs7320871	1.1E+08	T	0.976805	0.086493	0.019087	5.85E-06	323456	0.980988	0.085762	0.019088	7.02E-06	-0.00598
7	rs1811878	1.18E+08	A	0.999001	-0.39951	0.089957	8.95E-06	330574	0.999549	-0.40092	0.089964	8.33E-06	-0.00778
7	rs6247737	1.19E+08	T	0.964049	-0.06564	0.014383	5.03E-06	372376	0.9675	-0.06596	0.014384	4.52E-06	-0.00032
7	rs2836417	1.23E+08	G	0.997189	-0.22428	0.048867	4.44E-06	398845	0.99765	-0.22476	0.048868	4.24E-06	0
7	rs1215542	1.4E+08	C	0.720675	0.030453	0.006081	5.50E-07	358669	0.720628	0.030453	0.006081	5.50E-07	0
7	rs7916951	1.59E+08	C	0.890545	0.038939	0.008782	9.24E-06	355172	0.893584	0.038939	0.008782	9.25E-06	0
8	rs1459755	1691648	G	0.993237	-0.14993	0.032854	5.03E-06	369354	0.993227	-0.14993	0.032855	5.03E-06	0
8	rs5560653	49044127	A	0.999432	-0.50286	0.111767	6.82E-06	377648	0.9997	-0.5137	0.111794	4.33E-06	0.023358
8	rs1384228	57983018	G	0.98418	0.107686	0.023783	5.96E-06	304078	0.987918	0.109977	0.023789	3.78E-06	0
8	rs1865442	69574165	C	0.819279	-0.0518	0.00702	1.60E-13	366950	0.823937	-0.04726	0.007067	2.27E-11	-0.11614
8	rs1693488	69580086	A	0.93686	0.070132	0.011331	6.03E-10	352608	0.939394	0.061207	0.011406	8.03E-08	-0.00478
8	rs7668932	78191855	C	0.999051	-0.43788	0.093076	2.54E-06	326047	0.99935	-0.43125	0.093082	3.60E-06	0
8	rs1268085	95582655	A	0.682713	0.029176	0.005853	6.21E-07	360846	0.688986	0.029176	0.005853	6.22E-07	0
8	rs7814941	1.31E+08	A	0.797514	0.045687	0.006798	1.81E-11	358807	0.799258	0.045687	0.006799	1.82E-11	0
8	8:1426020	1.43E+08	C	0.998375	-0.31196	0.066818	3.03E-06	369726	0.998998	-0.31196	0.06682	3.03E-06	0
9	rs2938908	81144448	C	0.03306	0.070568	0.015066	2.81E-06	369771	0.031552	0.070568	0.015066	2.82E-06	0
9	rs1911935	99085533	T	0.997496	-0.27232	0.054826	6.80E-07	357363	0.998296	-0.27232	0.054828	6.81E-07	0
9	rs1098343	1.2E+08	G	0.786479	0.033659	0.006692	4.92E-07	356739	0.79196	0.033704	0.006692	4.75E-07	0.001494
9	rs5432206	1.25E+08	A	0.999258	-0.45483	0.100858	6.50E-06	355735	0.999549	-0.45559	0.100861	6.27E-06	0
9	rs1150768	1.4E+08	C	0.875793	-0.03689	0.008166	6.27E-06	369847	0.877802	-0.03689	0.008167	6.28E-06	0

Supplementary Table 4A. The 99% credible set for replicated SNPs implicated as genome-wide significant and independent by COJO analysis with proxies.

chr	pos	rsid	locus_id	Posterior_Prob	above_threshold
8	130717716	rs10956487	rs10956487	1	TRUE
8	130719718	rs7816131	rs10956487	1	TRUE
8	130724556	rs12679359	rs10956487	1	TRUE
8	130725665	rs6470764	rs10956487	1	TRUE
8	130735460	rs60228607	rs10956487	1	TRUE
8	130737391	rs3886937	rs10956487	1	TRUE
8	130756634	rs76634218	rs10956487	1	TRUE
8	130718712	rs4130415	rs10956487	NA	proxy
8	130718772	rs7833174	rs10956487	NA	proxy
8	130719623	rs7816342	rs10956487	NA	proxy
8	130723792	rs6651255	rs10956487	NA	proxy
8	130718020	rs10808583	rs10956487	NA	proxy
8	130718859	rs7814941	rs10956487	NA	proxy
8	130719567	rs7815955	rs10956487	NA	proxy
8	130721419	rs59912996	rs10956487	NA	proxy
8	130721421	rs116662391	rs10956487	NA	proxy
8	130723728	rs4733724	rs10956487	NA	proxy
8	130721749	rs35264025	rs10956487	NA	proxy
8	130728361	rs6986256	rs10956487	NA	proxy
8	130730280	rs11984666	rs10956487	NA	proxy
8	130731244	rs10956490	rs10956487	NA	proxy
8	130731376	rs4733725	rs10956487	NA	proxy
8	130731402	rs4733726	rs10956487	NA	proxy
8	130732739	rs7815298	rs10956487	NA	proxy
8	130733847	rs66937183	rs10956487	NA	proxy
8	130734461	rs2062078	rs10956487	NA	proxy
8	130736697	rs6470765	rs10956487	NA	proxy
8	130736929	rs6985118	rs10956487	NA	proxy
8	130737546	rs3886938	rs10956487	NA	proxy
8	130737601	rs1074286	rs10956487	NA	proxy
8	130738457	rs4733732	rs10956487	NA	proxy
8	130738972	rs7826493	rs10956487	NA	proxy
8	130721793	rs35383270	rs10956487	NA	proxy
8	130735330	rs7841981	rs10956487	NA	proxy
8	130721420	rs10087031	rs10956487	NA	proxy
8	130729518	rs4368942	rs10956487	NA	proxy
8	130735662	rs28743107	rs10956487	NA	proxy
8	130719436	rs10585686	rs10956487	NA	proxy
8	130719443	rs79164994	rs10956487	NA	proxy
8	130720646	rs6470763	rs10956487	NA	proxy
8	130739528	rs6470768	rs10956487	NA	proxy
8	130739657	rs6470769	rs10956487	NA	proxy
8	130740135	rs7011557	rs10956487	NA	proxy
8	130740400	rs7012062	rs10956487	NA	proxy
8	130740522	rs7012249	rs10956487	NA	proxy
8	130740650	rs6994279	rs10956487	NA	proxy
8	130740779	rs6998296	rs10956487	NA	proxy
8	130740859	rs7016313	rs10956487	NA	proxy
8	130740898	rs6998472	rs10956487	NA	proxy
8	130741042	rs10109335	rs10956487	NA	proxy
8	130741139	rs10956491	rs10956487	NA	proxy
8	130741183	rs7017052	rs10956487	NA	proxy
8	130741320	rs7017235	rs10956487	NA	proxy
8	130741938	rs6470770	rs10956487	NA	proxy
8	130742257	rs6984575	rs10956487	NA	proxy
8	130743547	rs7839339	rs10956487	NA	proxy
8	130743801	rs6470773	rs10956487	NA	proxy
8	130745178	rs4613961	rs10956487	NA	proxy
8	130745471	rs58825840	rs10956487	NA	proxy
8	130745576	rs6983071	rs10956487	NA	proxy
8	130746029	rs117091376	rs10956487	NA	proxy
8	130746030	rs118087346	rs10956487	NA	proxy
8	130746031	rs150622382	rs10956487	NA	proxy
8	130746035	rs140880131	rs10956487	NA	proxy
8	130747251	rs4733733	rs10956487	NA	proxy
8	130747520	rs112521609	rs10956487	NA	proxy
8	130749240	rs112292430	rs10956487	NA	proxy
8	130749290	rs113699963	rs10956487	NA	proxy
8	130749375	rs189933136	rs10956487	NA	proxy
8	130751015	rs4360262	rs10956487	NA	proxy
8	130751025	rs4584118	rs10956487	NA	proxy
8	130751292	rs57192532	rs10956487	NA	proxy
8	130752372	rs4366050	rs10956487	NA	proxy
8	130752408	rs4633026	rs10956487	NA	proxy
8	130752725	rs4367506	rs10956487	NA	proxy
8	130753603	rs7844275	rs10956487	NA	proxy
8	130753742	rs4559213	rs10956487	NA	proxy
8	130754719	rs4733737	rs10956487	NA	proxy
8	130754887	rs4236748	rs10956487	NA	proxy
8	130756531	rs1989396	rs10956487	NA	proxy

8	130757584	rs4509279	rs10956487	NA	proxy
8	130757769	rs34207831	rs10956487	NA	proxy
8	130757820	rs61199848	rs10956487	NA	proxy
8	130759579	rs6470778	rs10956487	NA	proxy
8	130759766	rs61503621	rs10956487	NA	proxy
8	130759999	rs4733738	rs10956487	NA	proxy
8	130736854	rs6470766	rs10956487	NA	proxy
8	130743745	rs6470772	rs10956487	NA	proxy
8	130755205	rs4128895	rs10956487	NA	proxy
8	130743726	rs6470771	rs10956487	NA	proxy
8	130730155	rs77629490	rs10956487	NA	proxy
8	130732447	rs57931547	rs10956487	NA	proxy
8	130738680	rs76623896	rs10956487	NA	proxy
8	130742202	rs74491503	rs10956487	NA	proxy
8	130742739	rs75439945	rs10956487	NA	proxy
8	130759089	rs58099650	rs10956487	NA	proxy
8	130759156	rs78291782	rs10956487	NA	proxy
8	130762291	rs77681114	rs10956487	NA	proxy
8	130729821	rs117981565	rs10956487	NA	proxy
8	130742028	rs74373572	rs10956487	NA	proxy
8	130745832	rs150496402	rs10956487	NA	proxy
8	130746292	rs78691434	rs10956487	NA	proxy
8	130754340	rs75020681	rs10956487	NA	proxy
8	130756975	rs79549681	rs10956487	NA	proxy
8	130758259	rs78738626	rs10956487	NA	proxy
10	73741706	rs2091331	rs2219837	1	TRUE
10	73745476	rs1006974	rs2219837	1.00E+00	TRUE
10	73764509	rs6480592	rs2219837	1	TRUE
10	73802875	rs1269600	rs2219837	1	TRUE
10	73805812	rs1668159	rs2219837	1	TRUE
10	73825652	rs1668169	rs2219837	1	TRUE
10	73832859	rs896074	rs2219837	1	TRUE
10	73744470	rs2394847	rs2219837	NA	proxy
10	73745599	rs2127357	rs2219837	NA	proxy
10	73738409	rs11000123	rs2219837	NA	proxy
10	73744948	rs4746103	rs2219837	NA	proxy
10	73744987	rs4746104	rs2219837	NA	proxy
10	73747388	rs11000125	rs2219837	NA	proxy
10	73752005	rs4747231	rs2219837	NA	proxy
10	73757768	rs6480591	rs2219837	NA	proxy
10	73758092	rs4148930	rs2219837	NA	proxy
10	73756149	rs113679580	rs2219837	NA	proxy
10	73740613	rs4148928	rs2219837	NA	proxy
10	73740837	rs4148929	rs2219837	NA	proxy
10	73741959	rs2091332	rs2219837	NA	proxy
10	73755778	rs7085958	rs2219837	NA	proxy
10	73732665	rs10762498	rs2219837	NA	proxy
10	73737124	rs4148926	rs2219837	NA	proxy
10	73744118	rs10400065	rs2219837	NA	proxy
10	73750461	rs2394849	rs2219837	NA	proxy
10	73737913	rs12258400	rs2219837	NA	proxy
10	73737206	rs549995569	rs2219837	NA	proxy
10	73733952	rs4284332	rs2219837	NA	proxy
10	73758332	rs730334	rs2219837	NA	proxy
10	73760176	rs7907616	rs2219837	NA	proxy
10	73759794	rs4148932	rs2219837	NA	proxy
10	73759890	rs4148933	rs2219837	NA	proxy
10	73761015	rs751450	rs2219837	NA	proxy
10	73762673	rs2219837	rs2219837	NA	proxy
10	73751693	rs538140606	rs2219837	NA	proxy
10	73780524	rs10546649	rs2219837	NA	proxy
10	73777618	rs66975633	rs2219837	NA	proxy
10	73777701	rs5786059	rs2219837	NA	proxy
10	73768992	rs4148941	rs2219837	NA	proxy
10	73770073	rs4148946	rs2219837	NA	proxy
10	73770651	rs4148949	rs2219837	NA	proxy
10	73772161	rs1871451	rs2219837	NA	proxy
10	73772661	rs1871452	rs2219837	NA	proxy
10	73796152	rs1245527	rs2219837	NA	proxy
10	73780494	rs1245580	rs2219837	NA	proxy
10	73782022	rs11000138	rs2219837	NA	proxy
10	73782236	rs7895905	rs2219837	NA	proxy
10	73778267	rs1245582	rs2219837	NA	proxy
10	73784025	rs1245518	rs2219837	NA	proxy
10	73783273	rs11334290	rs2219837	NA	proxy
10	73787602	rs1245524	rs2219837	NA	proxy
10	73788533	rs1271934	rs2219837	NA	proxy
10	73789033	rs1245535	rs2219837	NA	proxy
10	73804642	rs1668158	rs2219837	NA	proxy
10	73806570	rs1668160	rs2219837	NA	proxy
10	73806788	rs1668161	rs2219837	NA	proxy
10	73806909	rs1678619	rs2219837	NA	proxy
10	73807231	rs1668162	rs2219837	NA	proxy

10	73807828	rs1245573	rs2219837	NA	proxy
10	73810670	rs1245576	rs2219837	NA	proxy
10	73812476	rs1871453	rs2219837	NA	proxy
10	73807237	rs148395181	rs2219837	NA	proxy
10	73814545	rs4747238	rs2219837	NA	proxy
10	73807414	rs7913636	rs2219837	NA	proxy
10	73817772	rs1618927	rs2219837	NA	proxy
10	73798873	rs1271351	rs2219837	NA	proxy
10	73820001	rs1049269	rs2219837	NA	proxy
10	73822025	rs1049246	rs2219837	NA	proxy
10	73823019	rs1668172	rs2219837	NA	proxy
10	73825810	rs1668168	rs2219837	NA	proxy
10	73820622	rs3180	rs2219837	NA	proxy
10	73824181	rs2242251	rs2219837	NA	proxy
10	73824203	rs2242252	rs2219837	NA	proxy
10	73801887	rs1245512	rs2219837	NA	proxy
10	73834618	rs1245569	rs2219837	NA	proxy
10	73837341	rs1245562	rs2219837	NA	proxy
10	73834788	rs1245568	rs2219837	NA	proxy
10	73835158	rs1245567	rs2219837	NA	proxy
10	73835649	rs1245566	rs2219837	NA	proxy
10	73835968	rs1245565	rs2219837	NA	proxy
10	73836952	rs1245563	rs2219837	NA	proxy
10	73837016	rs1268456	rs2219837	NA	proxy
10	73837350	rs1245561	rs2219837	NA	proxy
10	73826335	rs1678626	rs2219837	NA	proxy
10	73838264	rs1245559	rs2219837	NA	proxy
12	23936398	rs7977132	rs9804988	5.06E-02	TRUE
12	23960729	rs11831278	rs9804988	1.28E-01	TRUE
12	23972014	rs56290807	rs9804988	1.16E-01	TRUE
12	23973832	rs2955526	rs9804988	1.00E+00	TRUE
12	23973837	rs2955527	rs9804988	1.00E+00	TRUE
12	23974404	rs12308843	rs9804988	1.00E+00	TRUE
12	23975219	rs12310519	rs9804988	5.03E-01	TRUE
12	23975953	rs11834194	rs9804988	4.16E-01	TRUE
12	23977474	rs12581539	rs9804988	2.52E-01	TRUE
12	23978200	rs7134575	rs9804988	1.53E-01	TRUE
12	23982559	rs9804988	rs9804988	2.05E-01	TRUE
12	23947697	rs34616559	rs9804988	NA	proxy
12	23974911	rs149240432	rs9804988	NA	proxy

Supplementary Table 4B. Summary from analysis of variants from 99% credible set with variant effect predictor (VEP).

#Uploaded variation	Location	Allele	Consequence	IMPACT	SYMBOL	Gene	Feature_type	Feature	BIOPTYPE	EXON	INTRON	Existing_variation	DISTANCE	CANONICAL	TSL	APPRIS	ENSP	SIFT	PolyPhen	CLIN	SIG	PHENO	PUBMED	LoFTool	Condel
r\$10762498	1071972907-71972907	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs10762498	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4284332	1071974194-71974194	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4284332	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4284332	1071974194-71974194	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs4284332	-	YES	-	-	-	-	-	-	-	-	-	-		
rs4148926	1071977366-71977366	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4148926	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4148926	1071977366-71977366	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs4148926	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4148926	1071977366-71977366	T	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs4148926	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs549995569	1071977448-71977450	-	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs549995569	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$12258400	1071978155-71978155	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs12258400	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs12258400	1071978155-71978155	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	enhancer	-	rs12258400	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$11000123	1071978651-71978651	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs11000123	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$11000123	1071978651-71978651	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs11000123	-	YES	-	-	-	-	-	-	-	-	-	-		
rs4148928	1071980855-71980855	A	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4148928	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4148928	1071980855-71980855	A	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs4148928	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4148929	1071981079-71981079	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4148929	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
rs4148929	1071981079-71981079	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs4148929	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$2091331	1071981948-71981948	G	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs2091331	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$2091331	1071981948-71981948	G	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029646	promoter	-	rs2091331	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$2091332	1071982201-71982201	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs2091332	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1040065	1071984360-71984360	A	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs1040065	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1040065	1071984360-71984360	A	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs1040065	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1040065	1071984360-71984360	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs1040065	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$2394847	1071984712-71984712	G	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs2394847	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$2394847	1071984712-71984712	G	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs2394847	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$2394847	1071984712-71984712	G	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs2394847	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$2394847	1071984712-71984712	T	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs2394847	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$2394847	1071984712-71984712	T	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs2394847	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$2394847	1071984712-71984712	T	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs2394847	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$4746103	1071985190-71985190	A	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4746103	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4746103	1071985190-71985190	G	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4746103	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4746103	1071985190-71985190	G	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs4746103	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4746103	1071985190-71985190	G	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs4746103	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4746103	1071985190-71985190	G	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs4746103	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4746104	1071985228-71985228	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4746104	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4746104	1071985228-71985228	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs4746104	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$1006974	1071985718-71985718	T	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs1006974	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1006974	1071985718-71985718	T	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs1006974	-	YES	-	-	-	-	-	-	-	-	-	-		
r\$2127357	1071985841-71985841	T	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs2127357	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$2127357	1071985841-71985841	T	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs2127357	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1100125	1071986730-71986730	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs1100125	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1100125	1071986730-71986730	C	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs1100125	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1100125	1071986730-71986730	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs1100125	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$1100125	1071986730-71986730	C	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs1100125	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$538140606	1071991936-71991936	A	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs538140606	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$538140606	1071991936-71991936	A	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	promoter	-	rs538140606	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4747231	107199247-7199247	G	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4747231	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$4747231	107199247-7199247	G	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs4747231	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$7089584	1071996020-71996020	A	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	rs7089584	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$7089584	1071996020-71996020	A	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650	open_chromosome	-	rs7089584	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$113679580	1071996391-71996391	TCTT	intron_variant	MODIFIER	CHST3	ENSG00000122863	Transcript	ENST00000373115	protein_coding	1/2	r\$113679580	-	YES	1 P1	ENSP0000	-	-	-	-	-	-	-	0.133		
r\$113679580	1071996391-71996391	TCTT	regulatory_region_variant	MODIFIER	-	-	RegulatoryFeature	ENSR0000029650																	

rs11000138	1072022264-72022264	C	intergenic_variant	MODIFIER	-	-	-	-	-	-	rs11000138	-	-	-	-	-	-	-	-	-	-	-			
rs11000138	1072022264-72022264	T	intergenic_variant	MODIFIER	-	-	-	-	-	-	rs11000138	-	-	-	-	-	-	-	-	-	-	-			
rs7895905	1072022476-72022478	A	intergenic_variant	MODIFIER	-	-	-	-	-	-	rs7895905	-	-	-	-	-	-	-	-	-	-	-			
rs11334290	1072023515-2023516	intergenic_variant	MODIFIER	-	-	-	-	-	-	rs11334290	-	-	-	-	-	-	-	-	-	-	-				
rs1245516	1072024267-72024267	G	intergenic_variant	MODIFIER	-	-	-	-	-	-	rs1245516	-	-	-	-	-	-	-	-	-	-	-			
rs1245524	1072027844-72027844	G	regulatory_region_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029659	open_chrc	-	-	-	-	-	-	-	-	-	-	-			
rs1245524	1072027844-72027844	G	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029659	open_chrc	-	-	-	-	-	-	-	-	-	-	-			
rs1271394	1072028775-72028775	G	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029659	open_chrc	-	-	-	-	-	-	-	-	-	-	-			
rs1245535	1072029275-72029275	G	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029659	open_chrc	-	-	-	-	-	-	-	-	-	-	-			
rs1245527	1072036394-72036394	C	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029659	open_chrc	-	-	-	-	-	-	-	-	-	-	-			
rs1245527	1072036394-72036394	T	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029659	open_chrc	-	-	-	-	-	-	-	-	-	-	-			
rs1271391	1072039115-72039115	G	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1271391	1072039115-72039115	T	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1271391	1072042115-72042115	A	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1269600	1072043117-72043117	C	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668158	1072044884-72044884	G	regulatory_region_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668158	1072044884-72044884	T	regulatory_region_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668158	1072044884-72044884	G	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668158	1072044884-72044884	T	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668159	1072046054-72046054	T	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668160	1072046812-72046812	C	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668161	1072047030-72047030	A	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1678619	1072047151-72047151	C	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668162	1072047473-72047473	A	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs1668162	1072047473-72047473	T	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs148395181	1072047479-72047479	AATAAA	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs148395181	1072047479-72047479	AATAAAA	intergenic_variant	MODIFIER	-	-	-	-	RegulatoryFeature	ENSG0000029664	enhancer	-	-	-	-	-	-	-	-	-	-	-			
rs7913636	1072047656-72047656	A	intergenic_variant	MODIFIER	-	-	-	-	lncRNA	-	rs7913636	-	-	-	-	-	-	-	-	-	-	-			
rs7913636	1072047656-72047656	C	intergenic_variant	MODIFIER	-	-	-	-	lncRNA	-	rs7913636	-	-	-	-	-	-	-	-	-	-	-			
rs1245573	1072048070-72048070	A	intergenic_variant	MODIFIER	-	-	-	-	lncRNA	-	rs1245573	-	-	-	-	-	-	-	-	-	-	-			
rs1245573	1072048070-72048070	C	intergenic_variant	MODIFIER	-	-	-	-	lncRNA	-	rs1245573	-	-	-	-	-	-	-	-	-	-	-			
rs1245576	1072050912-72050912	A	downstream_gene_variant	MODIFIER	AC02239	ENSG00000272988	Transcript	ENST00000609403	lincRNA	-	rs1245576	238Z YES	-	-	-	-	-	-	-	-	-	-	-		
rs1245576	1072050912-72050912	C	downstream_gene_variant	MODIFIER	AC02239	ENSG00000272988	Transcript	ENST00000609403	lincRNA	-	rs1245576	238Z YES	-	-	-	-	-	-	-	-	-	-	-		
rs1871453	1072052118-72052118	C	downstream_gene_variant	MODIFIER	AC02239	ENSG00000272988	Transcript	ENST00000609403	lincRNA	-	rs1871453	576 YES	-	-	-	-	-	-	-	-	-	-	-		
rs4747238	1072054787-72054787	C	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST0000317376	protein_cds	-	rs4747238	4248 -	1 P2	ENSP000	-	-	-	-	-	-	-	-	0 184	-	
rs4747238	1072054787-72054787	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST0000317376	protein_cds	-	rs4747238	4248 -	1 P2	ENSP000	-	-	-	-	-	-	-	-	0.184	-	
rs4747238	1072054787-72054787	C	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST0000317376	protein_cds	-	rs4747238	4248 YES	1 P2	ENSP000	-	-	-	-	-	-	-	-	0.184	-	
rs4747238	1072054787-72054787	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST0000317376	protein_cds	-	rs4747238	4248 YES	1 P2	ENSP000	-	-	-	-	-	-	-	-	0.184	-	
rs4747238	1072054787-72054787	C	upstream_gene_variant	MODIFIER	AC02239	ENSG00000272988	Transcript	ENST00000609403	lincRNA	-	rs4747238	750 YES	-	-	-	-	-	-	-	-	-	-	-		
rs4747238	1072054787-72054787	G	upstream_gene_variant	MODIFIER	AC02239	ENSG00000272988	Transcript	ENST00000609403	lincRNA	-	rs4747238	750 YES	-	-	-	-	-	-	-	-	-	-	-		
rs1618927	1072058014-72058014	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST0000317376	protein_cds	-	rs1618927	1021 -	1 P2	ENSP000	-	-	-	-	-	-	-	-	0.184	-	
rs1618927	1072058014-72058014	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST0000317370	protein_cds	-	rs1618927	1021 YES	1 P2	ENSP000	-	-	-	-	-	-	-	-	0.184	-	
rs1618927	1072058014-72058014	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000460053	processed	-	rs1618927	4989 -	5	-	-	-	-	-	-	-	-	-	0.184	-	
rs1618927	1072058014-72058014	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000463279	processed	-	rs1618927	4791 -	5	-	-	-	-	-	-	-	-	-	0.184	-	
rs1618927	1072058014-72058014	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000469121	processed	-	rs1618927	4850 -	3	-	-	-	-	-	-	-	-	-	0.184	-	
rs1618927	1072058014-72058014	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000536168	protein_cds	-	rs1618927	4392 -	5 A2	ENSP000	-	-	-	-	-	-	-	-	0.184	-	
rs1049269	1072060243-72060243	G	3_prime_UTR_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000609403	lincRNA	-	rs1618927	3977 YES	-	-	-	-	-	-	-	-	-	-	-		
rs1049269	1072060243-72060243	G	3_prime_UTR_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000609403	lincRNA	-	rs1049269	4212 -	1 P2	ENSP000	-	-	-	-	-	-	-	23897914	0.184	-	
rs1049269	1072060243-72060243	G	3_prime_UTR_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000317376	protein_cds	-	rs1049269	2621 -	3	-	-	-	-	-	-	-	-	-	23897914	0.184	-
rs1049269	1072060243-72060243	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000536168	protein_cds	-	rs1049269	2163 -	5 A2	ENSP000	-	-	-	-	-	-	-	23897914	0.184	-	
rs3180	1072060684-72060684	G	3_prime_UTR_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000317376	protein_cds	-	rs3180	3180 -	1 P2	ENSP000	-	-	-	-	-	-	-	0.184	-	-	
rs3180	1072060684-72060684	G	3_prime_UTR_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000317370	protein_cds	-	rs3180	11/11	1 P2	ENSP000	-	-	-	-	-	-	-	0.184	-	-	
rs3180	1072060684-72060684	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000460053	processed	-	rs3180	2139 -	5	-	-	-	-	-	-	-	-	-	0.184	-	-
rs3180	1072060684-72060684	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000463279	processed	-	rs3180	1941 -	5	-	-	-	-	-	-	-	-	-	0.184	-	-
rs3180	1072060684-72060684	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000469121	processed	-	rs3180	2000 -	3	-	-	-	-	-	-	-	-	-	0.184	-	-
rs3180	1072060684-72060684	G	downstream_gene_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000536168	protein_cds	-	rs3180	1542 -	5 A2	ENSP000	-	-	-	-	-	-	-	0.184	-	-	
rs1049246	1072062267-7202267	G	3_prime_UTR_variant	MODIFIER	SPOCK2	ENSG00000107742	Transcript	ENST00000317376	protein_cds	-	rs1049246	-	1 P2	ENSP000	-	-	-	-	-	-	-	0.184	-	-	
rs1049246	1072062																								

rs1503621	8:12974290-129747520	G	downstream_gene_variant	MODIFIER	GSDMC	ENSG00000147697	Transcript	ENST00000169463	protein_coding	-	rs1503621	677	-	2P1	ENSP000K-	-	-	-	0.959-
rs473738	8:129747753-129747753	A	downstream_gene_variant	MODIFIER	GSDMC	ENSG00000147697	Transcript	ENST00000276708	protein_coding	-	rs473738	443	YES	1P1	ENSP000K-	-	-	-	0.959-
rs473738	8:129747753-129747753	A	downstream_gene_variant	MODIFIER	GSDMC	ENSG00000147697	Transcript	ENST00000521365	retained_intron	-	rs473738	3955	-	3-	-	-	-	-	0.959-
rs473738	8:129747753-129747753	A	downstream_gene_variant	MODIFIER	GSDMC	ENSG00000147697	Transcript	ENST00000522273	retained_intron	-	rs473738	443	-	1-	-	-	-	-	0.959-
rs7766114	8:129750045-129750045	A	synonymous_variant	LOW	GSDMC	ENSG00000147697	Transcript	ENST00000276708	protein_coding	12/14	rs7766114	-	YES	1P1	ENSP000K-	-	-	-	0.959-
rs7766114	8:129750045-129750045	A	downstream_gene_variant	MODIFIER	GSDMC	ENSG00000147697	Transcript	ENST00000251265	retained_intron	-	rs7766114	1663	-	3-	-	-	-	-	0.959-
rs7766114	8:129750045-129750045	A	non_coding_transcript_exon_variant	MODIFIER	GSDMC	ENSG00000147697	Transcript	ENST00000521365	retained_intron	6/8	rs7766114	-	-	1-	-	-	-	-	0.959-
rs7766114	8:129750045-129750045	A	synonymous_variant	LOW	GSDMC	ENSG00000147697	Transcript	ENST00000619463	protein_coding	11/13	rs7766114	-	-	2P1	ENSP000K-	-	-	-	0.959-

Supplementary Table 4C. Summary from analysis of variants from 99% credible set with RegulomeDB

#chromosome	coordinate	rsid	hits	score
chr8	130735459	rs60228607	Motifs PWM MECF	2b
chr8	130719566	rs7815955	Motifs Footprinting	2b
chr8	130721419	rs10087031	Motifs PWM Zfp10	2b
chr8	130721420	rs116662391	Motifs PWM Srf, N	2b
chr8	130721419	rs10087031	Motifs Footprinting	2b
chr8	130740858	rs7016313	Motifs Footprinting	2b
chr8	130740897	rs6998472	Motifs Footprinting	2b
chr8	130742201	rs74491503	Motifs Footprinting	2b
chr8	130719717	rs7816131	Motifs PWM PDX1	3a
chr8	130728360	rs6986256	Motifs PWM HMG	3a
chr8	130738456	rs4733732	Chromatin_Structu	4
chr8	130738971	rs7826493	Chromatin_Structu	4
chr8	130735329	rs7841981	Motifs Footprinting	4
chr8	130720645	rs6470763	Chromatin_Structu	4
chr8	130740778	rs6998296	Chromatin_Structu	4
chr8	130741041	rs10109335	Chromatin_Structu	4
chr8	130741138	rs10956491	Chromatin_Structu	4
chr8	130741182	rs7017052	Chromatin_Structu	4
chr8	130742256	rs6984575	Chromatin_Structu	4
chr8	130743546	rs7839339	Chromatin_Structu	4
chr8	130738679	rs76623896	Motifs Footprinting	4
chr8	130742027	rs74373572	Chromatin_Structu	4
chr8	130725664	rs6470764	Chromatin_Structu	5
chr8	130737390	rs3886937	Motifs PWM Sox1:	5
chr8	130719622	rs7816342	Motifs PWM Srf, C	5
chr8	130721749	rs35264025	Protein_Binding 02	5
chr8	130737545	rs3886938	Chromatin_Structu	5
chr8	130737600	rs1074286	Chromatin_Structu	5
chr8	130721793	rs35383270	Motifs PWM MEF-	5
chr8	130719436	rs10585686	Motifs PWM Srf, N	5
chr8	130719442	rs79164994	Motifs PWM Srf, N	5
chr8	130740134	rs7011557	Motifs Footprinting	5
chr8	130740399	rs7012062	Chromatin_Structu	5
chr8	130740521	rs7012249	Motifs PWM Gata	5
chr8	130740649	rs6994279	Chromatin_Structu	5
chr8	130741319	rs7017235	Protein_Binding C	5
chr8	130741937	rs6470770	Protein_Binding 01	5
chr8	130743800	rs6470773	Chromatin_Structu	5
chr8	130756530	rs1989396	Protein_Binding C	5
chr8	130759765	rs61503621	Motifs PWM PTF1	5
chr8	130759998	rs4733738	Motifs PWM delta	5
chr8	130736853	rs6470766	Chromatin_Structu	5
chr8	130743744	rs6470772	Motifs PWM Cutl1,	5
chr8	130743725	rs6470771	Chromatin_Structu	5
chr8	130742738	rs75439945	Protein_Binding C	5
chr8	130718858	rs7814941	Motifs PWM EWS	6
chr8	130731401	rs4733726	Motifs PWM TP53	6
chr8	130732738	rs7815298	Motifs PWM Freac	6
chr8	130733847	rs66937183	Motifs PWM GATA	6
chr8	130736696	rs6470765	Motifs PWM Foxk1	6
chr8	130736928	rs6985118	Motifs PWM DMR	6
chr8	130729517	rs4368942	Motifs PWM HOXC	6
chr8	130735661	rs28743107	Motifs PWM PU.1	6
chr8	130739527	rs6470768	Motifs PWM ZSCA	6
chr8	130745177	rs4613961	Motifs PWM NF-A	6
chr8	130745471	rs58825840	Motifs PWM SP1	6
chr8	130746028	rs117091376	Motifs PWM MyoD	6
chr8	130746029	rs118087346	Motifs PWM MyoD	6
chr8	130746031	rs150622382	Motifs PWM MyoD	6
chr8	130751292	rs57192532	Motifs PWM FOXC	6
chr8	130752407	rs4633026	Motifs PWM Glis2,	6
chr8	130753602	rs7844275	Motifs PWM Zfp28	6
chr8	130753741	rs4559213	Motifs PWM FOXF	6

chr8	130754886	rs4236748	Motifs PWM SPDE	6
chr8	130759578	rs6470778	Motifs PWM Hoxd	6
chr8	130755204	rs4128895	Motifs PWM Pou2l	6
chr8	130730154	rs77629490	Motifs PWM FOXC	6
chr8	130732446	rs57931547	Motifs PWM Oct-1	6
chr8	130759088	rs58099650	Motifs PWM Nano	6
chr8	130746291	rs78691434	Motifs PWM Duxl	6
chr8	130717715	rs10956487	No data	7
chr8	130724555	rs12679359	No data	7
chr8	130756633	rs76634218	No data	7
chr8	130718711	rs4130415	No data	7
chr8	130718771	rs7833174	No data	7
chr8	130723791	rs6651255	No data	7
chr8	130718019	rs10808583	No data	7
chr8	130723727	rs4733724	No data	7
chr8	130730279	rs11984666	No data	7
chr8	130731243	rs10956490	No data	7
chr8	130731375	rs4733725	No data	7
chr8	130734460	rs2062078	No data	7
chr8	130739656	rs6470769	No data	7
chr8	130745575	rs6983071	No data	7
chr8	130746034	rs140880131	No data	7
chr8	130747250	rs4733733	No data	7
chr8	130747519	rs112521609	No data	7
chr8	130749239	rs112292430	No data	7
chr8	130749289	rs113699963	No data	7
chr8	130749374	rs189933136	No data	7
chr8	130751014	rs4360262	No data	7
chr8	130751024	rs4584118	No data	7
chr8	130752371	rs4366050	No data	7
chr8	130752724	rs4367506	No data	7
chr8	130754718	rs4733737	No data	7
chr8	130757583	rs4509279	No data	7
chr8	130757769	rs34207831	No data	7
chr8	130757819	rs61199848	No data	7
chr8	130759155	rs78291782	No data	7
chr8	130762290	rs77681114	No data	7
chr8	130729820	rs117981565	No data	7
chr8	130745831	rs150496402	No data	7
chr8	130754340	rs75020681	No data	7
chr8	130756974	rs79549681	No data	7
chr8	130758258	rs78738626	No data	7
chr10	73741705	rs2091331	Single_Nucleotides	1d
chr10	73745475	rs1006974	Single_Nucleotides	1f
chr10	73744469	rs2394847	Single_Nucleotides	1f
chr10	73745598	rs2127357	Motifs Footprinting	2b
chr10	73744947	rs4746103	Motifs Footprinting	2b
chr10	73805811	rs1668159	Motifs PWM SZF1	3a
chr10	73802874	rs1269600	Chromatin_Structu	4
chr10	73738408	rs11000123	Motifs Footprinting	4
chr10	73744986	rs4746104	Motifs Footprinting	4
chr10	73764508	rs6480592	Chromatin_Structu	5
chr10	73825651	rs1668169	Motifs PWM MyoD	5
chr10	73832858	rs896074	Chromatin_Structu	5
chr10	73757767	rs6480591	Motifs PWM HEY1	5
chr10	73747387	rs11000125	No data	7
chr10	73752004	rs4747231	No data	7
chr10	73740836	rs4148929	Single_Nucleotides	1b
chr10	73740612	rs4148928	Single_Nucleotides	1f
chr10	73755777	rs7085958	Single_Nucleotides	1f
chr10	73732664	rs10762498	Single_Nucleotides	1f
chr10	73737123	rs4148926	Single_Nucleotides	1f
chr10	73758091	rs4148930	Related_Data meth	5
chr10	73756149	rs113679580	Chromatin_Structu	5
chr10	73741958	rs2091332	Chromatin_Structu	5
chr10	73744117	rs10400065	Motifs PWM ZIC1,	5
chr10	73737912	rs12258400	Motifs PWM RARC	6

chr10	73750460	rs2394849	No data	7
chr10	73759793	rs4148932	Motifs Footprinting	2b
chr10	73759889	rs4148933	Motifs Footprinting	2b
chr10	73761014	rs751450	Motifs Footprinting	2b
chr10	737733951	rs4284332	Motifs Footprinting	5
chr10	737758331	rs730334	Chromatin_Structu	5
chr10	737760175	rs7907616	Motifs PWM E2F3	5
chr10	737762672	rs2219837	Motifs PWM znf14	5
chr10	737787601	rs1245524	Motifs Footprinting	2a
chr10	73782021	rs11000138	Motifs PWM Srf, N	3a
chr10	737768991	rs4148941	Chromatin_Structu	4
chr10	737772660	rs1871452	Chromatin_Structu	4
chr10	737788532	rs1271934	Chromatin_Structu	4
chr10	73804641	rs1668158	Chromatin_Structu	4
chr10	737777618	rs66975633	Motifs PWM Zbtb3	5
chr10	73777701	rs5786059	Motifs PWM Srf, N	5
chr10	737770072	rs4148946	Chromatin_Structu	5
chr10	737770650	rs4148949	Chromatin_Structu	5
chr10	737772160	rs1871451	Chromatin_Structu	5
chr10	73782235	rs7895905	Motifs PWM HTF,	5
chr10	73806569	rs1668160	Chromatin_Structu	5
chr10	73810669	rs1245576	Chromatin_Structu	5
chr10	73812475	rs1871453	Chromatin_Structu	5
chr10	73780524	rs10546649	Motifs PWM Cart-	6
chr10	73784024	rs1245518	Motifs PWM INSM	6
chr10	73783273	rs11334290	Motifs PWM Srf, N	6
chr10	73806787	rs1668161	Motifs PWM mTEF	6
chr10	73806908	rs1678619	Motifs PWM C/EBI	6
chr10	73807230	rs1668162	Motifs PWM HNF8	6
chr10	73807827	rs1245573	Motifs Footprinting	6
chr10	73796151	rs1245527	No data	7
chr10	73780493	rs1245580	No data	7
chr10	737778266	rs1245582	No data	7
chr10	73789032	rs1245535	No data	7
chr10	73820000	rs1049269	Chromatin_Structu	4
chr10	73834617	rs1245569	Chromatin_Structu	4
chr10	73798872	rs1271351	Motifs Footprinting	5
chr10	73822204	rs1049246	Chromatin_Structu	5
chr10	73823018	rs1668172	Chromatin_Structu	5
chr10	73825809	rs1668168	Chromatin_Structu	5
chr10	73820621	rs3180	Chromatin_Structu	5
chr10	73824180	rs2242251	Chromatin_Structu	5
chr10	73824202	rs2242252	Chromatin_Structu	5
chr10	73837340	rs1245562	Motifs PWM WT1,	5
chr10	73834787	rs1245568	Chromatin_Structu	5
chr10	73835157	rs1245567	Motifs Footprinting	5
chr10	73835648	rs1245566	Chromatin_Structu	5
chr10	73835967	rs1245565	Motifs PWM NHLH	5
chr10	73837349	rs1245561	Motifs Footprinting	5
chr10	73826334	rs1678626	Motifs PWM TFE,	5
chr10	73807237	rs148395181	Motifs PWM FOXC	6
chr10	73814544	rs4747238	Motifs PWM Dlx3	6
chr10	73817771	rs1618927	Motifs PWM Gm38	6
chr10	73837015	rs1268456	Motifs PWM Nkx3-2	6
chr10	73838263	rs1245559	Motifs PWM Tcfap	6
chr10	73807413	rs7913636	No data	7
chr10	73801886	rs1245512	No data	7
chr10	73836951	rs1245563	No data	7
chr12	23960728	rs11831278	Motifs PWM HIC2	6
chr12	23972013	rs56290807	Motifs PWM Zfp12	6
chr12	23947696	rs34616559	Motifs PWM CDP,	6
chr12	23974910	rs149240432	Motifs PWM Six1,	6
chr12	23936397	rs7977132	No data	7
chr12	23973831	rs2955526	No data	7
chr12	23973836	rs2955527	No data	7
chr12	23974403	rs12308843	No data	7
chr12	23975218	rs12310519	No data	7

chr12	23975952	rs11834194	No data	7
chr12	23977473	rs12581539	No data	7
chr12	23978199	rs7134575	No data	7
chr12	23982558	rs9804988	No data	7

Supplementary Table 5. Results of univariate and COJO analyses of crude pain BP_MA 450K GWAS with p<5e-8.

Chr	SNP	bp	effA	freq	b	se	p	n	freq_geno	bJ	bJ_se	pJ	LD_r	
12	rs9804988	23982559	T		0.1304	0.0579	0.007	1.31E-16	471902	0.1305	0.0579	0.0070005	1.33E-16	0
8	rs10956487	130717716	A		0.7678	0.0444	0.0057	5.88E-15	454819	0.772467	0.0444	0.00570037	6.76E-15	0
8	rs72666766	69580612	A		0.8187	-0.0461	0.0061	5.77E-14	477004	0.821618	-0.0461	0.00610036	4.13E-14	0
10	rs2219837	73762673	T		0.3993	-0.0341	0.0049	2.51E-12	456205	0.393264	-0.0341	0.00490025	3.43E-12	0
10	rs2672596	124226793	A		0.255	-0.0363	0.0055	4.06E-11	457185	0.260704	-0.0360321	0.00550046	5.73E-11	0.00860254
6	rs6907508	34592090	A		0.8845	-0.0465	0.0074	3.07E-10	468235	0.883028	-0.0474226	0.00740204	1.49E-10	0
14	rs8022156	37657148	T		0.7338	0.0337	0.0054	4.80E-10	461104	0.74019	0.0337	0.00540022	4.36E-10	0
11	rs324300	29674831	A		0.3729	0.0287	0.0049	4.80E-09	467760	0.37225	0.0287	0.00490017	4.71E-09	0
5	rs10475978	170859228	C		0.4757	-0.0278	0.0048	5.34E-09	458114	0.477289	-0.0278	0.00480017	6.98E-09	0
8	rs12680855	95582655	A		0.6823	0.0295	0.0051	8.78E-09	467296	0.688986	0.0295	0.00510018	7.29E-09	0
9	rs11507683	140262424	T		0.1221	0.0414	0.0072	9.75E-09	474847	0.122198	0.0414	0.00720024	8.93E-09	0
10	rs10870267	133968063	T		0.5573	-0.0276	0.0048	9.78E-09	462214	0.564917	-0.027331	0.00480034	1.24E-08	0
18	rs7226995	50895755	A		0.4707	-0.0273	0.0048	9.86E-09	458164	0.470117	-0.0273	0.00480016	1.29E-08	0
5	rs1921117	30876763	A		0.386	0.028	0.0049	9.86E-09	462618	0.389251	0.028	0.00490017	1.10E-08	0
20	rs1204765	49719603	T		0.5237	-0.0268	0.0048	1.91E-08	458377	0.5234	-0.0268	0.00480016	2.36E-08	0
6	rs28732174	32081196	A		0.1048	0.0432	0.0077	2.00E-08	470926	0.101781	0.04427	0.00770206	9.04E-09	0.0217465
5	rs4703253	102892224	T		0.3171	-0.0288	0.0051	2.01E-08	467388	0.328076	-0.0288	0.00510017	1.63E-08	0
3	rs6779524	49450449	T		0.3065	-0.0289	0.0052	2.36E-08	458407	0.30133	-0.0289	0.00520017	2.74E-08	0
4	rs4974563	1138153	T		0.6933	0.0288	0.0052	2.44E-08	456670	0.693887	0.0288	0.00520017	3.05E-08	0
13	rs76134699	87294817	T		0.9875	0.1328	0.0239	2.93E-08	372037	0.992359	0.1328	0.023901	2.76E-08	0
11	rs1940720	112857202	A		0.6124	-0.027	0.0049	3.16E-08	460826	0.612873	-0.027	0.00490016	3.59E-08	0
4	rs13135092	103198082	A		0.9165	-0.0473	0.0086	3.49E-08	463905	0.916658	-0.0473	0.00860027	3.80E-08	0
4	rs189350593	140243320	A		0.9898	-0.1316	0.0239	3.81E-08	455304	0.991758	-0.1316	0.0239008	3.67E-08	0

Supplementary Table 6: Genetic correlations between BP_MA and different traits, as estimated by LD score regression.

PMID: PubMed ID of the manuscript reporting this trait GWAS

rg: estimate of the genetic correlation between frailty and the trait

se: standard error of above estimate

z: value of the Z-test statistic

p: p-value

h2: estimate of heritability of the trait

h2_se: standard error of above estimate

trait1	trait2	PMID	Category	ethnicity	rg	se	z	p	h2_obs	h2_obs_se	h2_int	h2_int_se	gcov_int	gcov_int_se
BP	Years of schooling	27225129	education	European	-0.4741	0.0221	-21.4942	1.76E-102	1.25E-01	0.0044	0.9283	0.0106	-2.69E-02	0.0066
BP	Age of first birth	27798627	reproductive	European	-0.4911	0.0295	-16.6404	3.55E-62	0.063	0.0037	0.9493	0.0084	-0.0089	6.10E-03
BP	Depressive symptoms	27089181	psychiatric	European	0.5379	0.0429	12.5414	4.43E-36	0.0467	0.004	1.0003	0.0079	0.0554	0.0065
BP	College completion	23722424	education	European	-0.513	0.041	-12.5134	6.31E-36	0.0779	0.0058	1.0212	0.0084	0.0055	0.0065
BP	Neuroticism	27089181	personality	European	0.3894	0.0328	11.8805	1.49E-32	0.0905	0.006	0.9806	0.0103	0.0523	0.0072
BP	Waist circumference	25673412	anthropom	European	0.2893	0.0262	11.0633	1.89E-28	1.22E-01	0.005	0.8404	0.0082	0.0055	0.006
BP	Obesity class 1	23563607	anthropom	European	0.2855	0.0277	10.3143	6.07E-25	0.2189	0.012	1.0119	0.0114	-4.10E-03	0.0072
BP	Insomnia	28604731	sleeping	European	0.459	0.0473	9.699	3.05E-22	0.0468	0.0048	1.0014	0.007	0.0585	0.0054
BP	Intelligence	28530673	cognitive	European	-0.3051	0.0326	-9.3528	8.54E-21	0.1916	0.0102	1.0024	0.0089	-0.0308	0.0057
BP	Overweight	23563607	anthropom	European	0.2859	0.0317	9.025	1.80E-19	0.1112	0.0067	1.0183	0.0095	-0.0058	0.0064
BP	Hip circumference	25673412	anthropom	European	0.2311	0.0258	8.9734	2.87E-19	0.1294	0.0057	0.8533	0.0085	0.0022	0.0061
BP	Body mass index	20935630	anthropom	European	0.238	0.0275	8.6392	5.66E-18	1.90E-01	0.0095	1.006	0.0111	7.00E-04	0.0065
BP	Sleep duration	27494321	sleeping	European	-0.3019	0.038	-7.9338	2.13E-15	0.0549	0.005	1.0194	0.0077	-0.0153	0.0052
BP	Waist-to-hip ratio	25673412	anthropom	European	0.2181	0.0284	7.6886	1.49E-14	1.13E-01	0.0072	0.919	0.0094	0.009	0.006
BP	Number of children ever born	27798627	reproductive	European	0.3109	0.0421	7.376	1.63E-13	0.0251	0.0019	0.9713	0.0071	-0.0025	0.0059
BP	Obesity class 2	23563607	anthropom	European	0.2574	0.0372	6.9213	4.47E-12	0.1892	0.0126	0.9979	0.0106	0.0019	0.0078
BP	Subjective well being	27089181	psychiatric	European	-0.313	0.0457	-6.8482	7.48E-12	0.0253	0.0022	0.9984	0.0081	-0.0104	0.006
BP	Ever vs never smoked	20418890	smoking_b	European	0.3034	0.0447	6.7886	1.13E-11	0.0718	0.0067	1.0003	0.0063	0.0074	0.0059
BP	Body fat	26833246	anthropom	Mixed	0.2689	0.0397	6.7777	1.22E-11	0.1069	0.0083	0.9015	0.0066	1.40E-03	0.0056
BP	Mothers age at death	27015805	aging	European	-0.4316	0.0674	-6.4055	1.50E-10	3.61E-02	0.0076	1.0134	0.0074	-0.0052	0.0057
BP	Major depressive disorder	22472876	psychiatric	European	0.3883	0.0631	6.1539	7.56E-10	0.1708	0.0275	1.0026	0.0066	-7.50E-03	0.0053
BP	Coronary artery disease	26343387	cardiomet	Mixed	0.1862	0.0331	5.6224	1.88E-08	0.0806	0.0058	1.043	0.0101	0.0033	0.0059
BP	Extreme bmi	23563607	anthropom	European	0.2511	0.046	5.4633	4.67E-08	0.7009	0.0615	1.0294	0.0121	-0.0012	0.0085
BP	Triglycerides	20686565	lipids	European	0.1994	0.0377	5.2961	1.18E-07	1.72E-01	0.031	0.9665	0.0185	-0.0119	0.0062
BP	Parents age at death	27015805	aging	European	-0.3799	0.0722	-5.2621	1.42E-07	0.0296	0.0074	1.0144	0.0068	-0.0104	0.0051
BP	HDL cholesterol	20686565	lipids	European	-0.1954	0.0377	-5.1853	2.16E-07	0.1305	0.0238	1.0532	0.0494	0.0036	0.0066
BP	Obesity class 3	23563607	anthropom	European	0.2822	0.0577	4.8885	1.02E-06	0.1178	0.0148	0.9852	0.0101	-4.00E-04	0.0076
BP	Childhood IQ	23358156	education	European	-0.3036	0.0631	-4.8106	1.50E-06	2.69E-01	0.0437	1.0035	0.0094	-5.00E-03	0.007
BP	Former vs Current smoker	20418890	smoking_b	European	-0.3379	0.0714	-4.7335	2.21E-06	0.0564	0.0103	1.0057	0.0065	0.0015	0.0053
BP	Lung cancer	27488534	cancer	European	0.3032	0.0655	4.6302	3.65E-06	0.3242	0.0706	1.0129	0.0079	-0.0036	0.0052
BP	Age at Menopause	26414677	reproductive	European	-0.1537	0.0353	-4.3591	1.31E-05	0.138	0.0159	0.9875	0.0145	0.0098	0.0054
BP	Fasting insulin main effect	22581228	glycemic	European	0.2331	0.0539	4.3216	1.55E-05	0.0697	0.0094	1.0147	0.0068	3.00E-04	0.0051
BP	Fathers age at death	27015805	aging	European	-0.2699	0.0636	-4.2416	2.22E-05	0.0389	0.0065	1.0201	0.0069	-0.0212	0.0051

	Threshold							4.44444E-05						
BP	HOMA-IR	20081858	glycemic	European	0.2687	0.0708	3.7931	1.00E-04	0.0697	0.0128	1.0021	0.0069	0.0054	0.0053
BP	Lung cancer (all)	24880342	cancer	European	0.3096	0.0802	3.862	1.00E-04	0.1276	0.031	1.0091	0.008	-0.0037	0.0062
BP	Excessive daytime sleepiness	27992416	sleeping	European	0.1741	0.0465	3.742	2.00E-04	0.0537	0.0052	1.0037	0.0074	3.40E-02	0.0057
BP	Squamous cell lung cancer	27488534	cancer	European	0.3252	0.0868	3.7484	2.00E-04	0.0382	0.0119	1.0105	0.0064	-0.0039	0.0049
BP	Rheumatoid Arthritis	24390342	autoimmu	European	0.1303	0.036	3.6195	3.00E-04	0.1633	0.0302	1.0225	0.0188	0.0102	0.006
BP	Attention deficit hyperactivity disorder	27663945	psychiatric	European	0.4571	0.1328	3.4422	6.00E-04	0.0698	0.0309	0.9942	0.0079	0.0029	0.0065
BP	Attention deficit hyperactivity disorder	27663945	psychiatric	European	0.4561	0.1321	3.4516	6.00E-04	0.071	0.0313	1.0087	0.008	0.003	0.0065
BP	Cigarettes smoked per day	20418890	smoking_b	European	0.2487	0.0763	3.2588	0.0011	5.50E-02	0.0153	1.0097	0.0069	0.0052	0.0047
BP	Attention deficit hyperactivity disorder	20732625	psychiatric	European	0.3869	0.122	3.1703	1.50E-03	0.2319	0.093	1.0065	0.0069	-0.0025	0.005
BP	Childhood obesity	22484627	anthropom	European	0.1468	0.0463	3.1679	1.50E-03	0.4151	0.0447	0.9253	0.008	0.0054	0.0059
BP	Leptin_not_adjBMI	26833098	hormone	European	0.1692	0.0541	3.1244	0.0018	0.1039	0.0154	0.9887	0.0071	0.0052	0.0054
BP	Description of average fatty acid chain length	27005778	metabolite	European	-0.2818	0.0906	-3.1106	0.0019	0.0893	0.0336	0.9865	0.0069	0.0018	0.0051
BP	Fasting glucose main effect	22581228	glycemic	European	0.1456	0.0468	3.1074	0.0019	0.0946	0.018	1.0036	0.0105	-3.90E-03	0.0055
BP	Lung cancer (squamous cell)	24880342	cancer	European	0.3814	0.1243	3.0684	0.0022	0.0472	0.0203	1.0077	0.0065	-0.0064	0.0056
BP	Age of smoking initiation	20418890	smoking_b	European	-0.2873	0.0958	-2.9989	2.70E-03	0.0595	0.0178	1.0009	0.0062	6.58E-05	0.0054
BP	Lung adenocarcinoma	27488534	cancer	European	0.2807	0.0966	2.9059	0.0037	0.0332	0.0121	1.0167	0.0068	-0.0026	0.0052
BP	Lumbar Spine bone mineral density	26367794	bone	Mixed	0.1384	0.0478	2.8981	0.0038	0.1253	0.015	0.9796	0.0083	0.001	0.0061
BP	Lumbar spine bone mineral density	22504420	bone	Mixed	0.1135	0.0406	2.7922	0.0052	0.2634	0.0249	1.016	0.0093	0.0019	0.0061
BP	Primary sclerosing cholangitis	27992413	autoimmu	Mixed	-0.172	0.0622	-2.7631	0.0057	0.4205	0.1668	0.9896	0.0164	0.0057	0.0066
BP	22:6 docosahexaenoic acid	27005778	metabolite	European	-0.2372	0.0859	-2.7607	5.80E-03	0.1286	0.0369	0.9952	0.0073	-0.0036	0.0051
BP	HbA1C	20858683	glycemic	European	0.1609	0.0589	2.7333	0.0063	0.0656	0.0126	1.0002	0.0079	-4.00E-04	0.0055
BP	Autism spectrum disorder	0	psychiatric	European	-0.1398	0.0515	-2.7134	6.70E-03	4.63E-01	0.0472	0.9623	0.0066	0.0045	0.0052
BP	LDL cholesterol	20686565	lipids	European	0.1472	0.0549	2.6829	0.0073	0.1034	0.0319	1.0589	0.0574	-0.0166	0.008
BP	Total Cholesterol	20686565	lipids	European	0.1087	0.041	2.6507	0.008	0.1363	0.0262	1.0224	0.0405	-1.64E-02	0.0075
BP	Type 2 Diabetes	22885922	glycemic	European	0.1181	0.0445	2.6509	0.008	0.0892	0.0095	1.0089	0.0078	0.0048	0.0061
BP	PGC cross-disorder analysis	23453885	psychiatric	European	0.1116	0.0429	2.601	0.0093	0.1742	0.0131	1.0108	0.0115	-0.0073	0.0081
BP	Ratio of bisallylic groups to total fatty acids	27005778	metabolite	European	-0.1694	0.0681	-2.4895	0.0128	2.62E-01	0.0979	0.9877	0.009	-0.0034	0.0058
BP	Average number of methylene group	27005778	metabolite	European	0.1902	0.08	2.3779	1.74E-02	0.1903	0.0797	0.998	0.0093	0.0015	0.0059
BP	Neo-openness to experience	21173776	personality	European	-0.1902	0.0806	-2.3593	0.0183	0.1078	0.0257	0.9919	0.0067	5.80E-03	0.0058
BP	Chronotype	27494321	sleeping	European	-0.073	0.0311	-2.3458	1.90E-02	0.1024	0.006	1.0119	0.0082	-0.0198	0.0051
BP	Total cholesterol in large HDL	27005778	metabolite	European	-0.1781	0.076	-2.3445	0.0191	1.00E-01	0.0279	1.008	0.0153	-2.00E-04	0.0054
BP	Acetate	27005778	metabolite	European	-0.2298	0.0983	-2.3378	1.94E-02	0.0478	0.0194	1.0034	0.0069	0.0059	0.0055
BP	Triglycerides in small HDL	27005778	metabolite	European	0.2026	0.0868	2.3344	0.0196	7.53E-02	0.0289	0.9955	0.0088	-1.00E-04	0.0053
BP	Celiac disease	20190752	autoimmu	European	-0.1537	0.066	-2.3308	1.98E-02	0.3124	0.0531	1.0657	0.012	0.0153	0.0084
BP	Average number of double bonds in a	27005778	metabolite	European	-0.1733	0.0751	-2.3071	2.10E-02	1.58E-01	0.0548	1.005	0.0085	-3.00E-04	0.0057
BP	Ratio of bisallylic groups to double bonds	27005778	metabolite	European	-0.1432	0.0621	-2.3065	0.0211	0.2891	0.1089	0.9787	0.01	-0.0018	0.0056
BP	Mean Thalamus	25607358	brain_volu	European	0.1721	0.0759	2.268	0.0233	0.1354	0.0372	0.9802	0.0067	-4.10E-03	0.0057
BP	Age at Menarche	25231870	reproducti	European	-0.0648	0.0287	-2.2598	2.38E-02	0.2036	0.01	0.9431	0.0119	-0.0092	0.0066
BP	Total cholesterol in medium HDL	27005778	metabolite	European	-0.2263	0.1027	-2.2033	0.0276	0.0565	0.0254	0.9995	0.0103	0.0048	0.0056
BP	Amyotrophic lateral sclerosis	27455348	neurologic	European	0.1663	0.0768	2.1644	3.04E-02	0.0501	0.0126	0.993	0.0065	-0.0028	0.005
BP	HOMA-B	20081858	glycemic	European	0.118	0.0554	2.1294	0.0332	0.0851	0.0142	0.9914	0.0075	0.0087	0.0047
BP	Total cholesterol in HDL	27005778	metabolite	European	-0.178	0.084	-2.1186	0.0341	0.0893	0.0284	1.0085	0.0137	-5.00E-04	0.0055
BP	Difference in height between childho	23449627	anthropom	European	0.1211	0.0572	2.1171	0.0342	0.3526	0.0543	0.9695	0.0087	-0.0086	0.0056

BP	Tyrosine	27005778	metabolite	European	0.1475	0.0707	2.0846	0.0371	0.0749	0.0286	0.9992	0.0076	-0.0038	0.0052
BP	Free cholesterol in large HDL	27005778	metabolite	European	-0.1505	0.0728	-2.0671	0.0387	0.1014	0.0274	1.009	0.0147	-0.0026	0.0055
BP	Free cholesterol in medium HDL	27005778	metabolite	European	-0.1633	0.0806	-2.0252	0.0429	0.0702	0.0237	0.9966	0.0091	0.0028	0.0053
BP	Triglycerides in small VLDL	27005778	metabolite	European	0.135	0.067	2.0154	0.0439	0.1282	0.0383	0.9901	0.0083	0.003	0.0054
BP	Mono-unsaturated fatty acids	27005778	metabolite	European	0.176	0.0876	2.0079	0.0447	0.1203	0.0413	0.983	0.0074	-0.0047	0.0054
BP	Cholesterol esters in large HDL	27005778	metabolite	European	-0.1415	0.0728	-1.9418	0.0522	0.1175	0.0305	1.0029	0.0151	-0.0011	0.0055
BP	Heart rate	23583979	haemotolq	Mixed	0.0715	0.0372	1.9218	0.0546	0.0858	0.0098	1.0088	0.0093	2.00E-04	0.0056
BP	Cholesterol esters in medium HDL	27005778	metabolite	European	-0.204	0.1067	-1.9108	5.60E-02	0.057	0.0282	1.0018	0.01	0.0039	0.0057
BP	Triglycerides in IDL	27005778	metabolite	European	0.1398	0.0739	1.8918	0.0585	0.1183	0.0367	1.0072	0.0143	-2.10E-03	0.0057
BP	Albumin	27005778	metabolite	European	-0.172	0.0927	-1.8551	6.36E-02	0.0637	0.0252	0.9871	0.0072	0.0022	0.0051
BP	Infant head circumference	22504419	anthropom	European	-0.1261	0.0691	-1.825	0.068	2.45E-01	0.045	0.9882	0.007	-0.0025	0.0061
BP	Triglycerides in medium VLDL	27005778	metabolite	European	0.1318	0.0727	1.8132	0.0698	0.1039	0.0317	0.9954	0.007	5.60E-03	0.0056
BP	Triglycerides in very small VLDL	27005778	metabolite	European	0.1165	0.0643	1.8118	0.07	1.55E-01	0.0402	0.9926	0.01	0.0013	0.0054
BP	Phospholipids in medium HDL	27005778	metabolite	European	-0.1387	0.0771	-1.7994	0.072	0.072	0.0237	0.9935	0.0085	0.0045	0.0054
BP	Chronic Kidney Disease	26831199	kidney	Mixed	0.1283	0.0718	1.7867	7.40E-02	0.0188	0.0066	1.0189	0.0104	-0.0086	0.0063
BP	Height_2010	20881960	anthropom	European	0.0475	0.0267	1.78	0.0751	0.2898	0.0159	1.0102	0.0171	-0.004	0.008
BP	Serum total triglycerides	27005778	metabolite	European	0.1171	0.0659	1.7775	0.0755	1.37E-01	0.038	0.9864	0.008	0.0039	0.0055
BP	Total lipids in large HDL	27005778	metabolite	European	-0.118	0.069	-1.7089	0.0875	0.1249	0.0304	1.0023	0.0156	-0.0028	0.0055
BP	Schizophrenia	25056061	psychiatric	Mixed	0.0468	0.0279	1.68	0.093	0.4624	0.0192	1.045	0.0137	0.0031	0.0077
BP	Concentration of large HDL particles	27005778	metabolite	European	-0.1118	0.068	-1.645	0.1	0.1266	0.0303	1.0012	0.0158	-0.0029	0.0055
BP	Phospholipids in medium VLDL	27005778	metabolite	European	0.112	0.0682	1.6419	0.1006	0.12	0.0347	0.9919	0.0072	0.0051	0.0053
BP	Omega-3 fatty acids	27005778	metabolite	European	-0.1315	0.0807	-1.63	0.1031	0.1556	0.0415	0.9895	0.008	-2.90E-03	0.0055
BP	Phospholipids in large VLDL	27005778	metabolite	European	0.1059	0.0653	1.6228	0.1046	1.24E-01	0.0331	0.9863	0.0075	0.0057	0.0055
BP	Total lipids in medium HDL	27005778	metabolite	European	-0.142	0.0888	-1.5992	0.1098	0.0651	0.0262	0.9959	0.0087	0.0034	0.0055
BP	ICV	25607358	brain_volu	European	-0.1262	0.0796	-1.5853	0.1129	0.1704	0.0459	1.0035	0.0069	-0.0021	0.0057
BP	Urate	23263486	other	European	0.0468	0.03	1.5624	0.1182	0.1806	0.0628	0.9475	0.056	0.0016	0.0062
BP	Phospholipids in large HDL	27005778	metabolite	European	-0.107	0.0687	-1.5574	0.1194	1.22E-01	0.0303	0.9998	0.0149	-0.0032	0.0055
BP	Triglycerides in large VLDL	27005778	metabolite	European	0.1036	0.0668	1.5509	0.1209	1.21E-01	0.0309	0.9851	0.0076	0.0072	0.0057
BP	Extreme waist-to-hip ratio	23563607	anthropom	European	0.1039	0.0676	1.5366	0.1244	0.3495	0.0603	0.9785	0.0088	0.0073	0.0082
BP	Omega-9 and saturated fatty acids	27005778	metabolite	European	0.1464	0.0953	1.5358	0.1246	0.0968	0.0433	0.9922	0.0077	-0.0038	0.0054
BP	Concentration of large VLDL particles	27005778	metabolite	European	0.1005	0.0663	1.5167	0.1293	0.1388	0.0363	0.971	0.0078	0.0057	0.0056
BP	Total lipids in medium VLDL	27005778	metabolite	European	0.0926	0.0612	1.514	0.13	0.1541	0.037	0.9799	0.0073	0.0048	0.0053
BP	Concentration of small VLDL particles	27005778	metabolite	European	0.0923	0.0613	1.5049	0.1323	0.1619	0.0398	0.9859	0.0086	0.0022	0.0052
BP	Total lipids in large VLDL	27005778	metabolite	European	0.0911	0.0605	1.5041	0.1325	0.1491	0.0331	0.9813	0.0077	0.0061	0.0054
BP	Cholesterol esters in large VLDL	27005778	metabolite	European	0.089	0.0594	1.4999	1.34E-01	0.1708	0.0366	0.9757	0.0079	0.0038	0.0051
BP	Total lipids in small VLDL	27005778	metabolite	European	0.09	0.0614	1.4667	0.1424	0.1556	0.0401	0.9878	0.0091	0.0013	0.0051
BP	Alzheimers disease	24162737	neurologic	European	0.1155	0.0797	1.4486	1.47E-01	0.0418	0.0222	1.0703	0.0328	0.0053	0.0062
BP	Extreme height	23563607	anthropom	European	0.0566	0.0392	1.4444	0.1486	1.2905	0.1165	1.0241	0.02	-6.90E-03	0.0108
BP	Isoleucine	27005778	metabolite	European	0.1261	0.0881	1.4314	0.1523	0.0667	0.0245	0.9976	0.0071	-0.002	0.0057
BP	Glutamine	27005778	metabolite	European	-0.1175	0.0825	-1.4247	0.1543	0.0649	0.0221	1.0172	0.0079	-4.00E-04	0.0051
BP	Phenylalanine	27005778	metabolite	European	0.1251	0.0884	1.4159	0.1568	0.0606	0.0219	1.0023	0.0069	0.0018	0.0053
BP	Free cholesterol in small VLDL	27005778	metabolite	European	0.0993	0.0703	1.4134	0.1575	0.1153	0.0368	0.9987	0.0097	0.0012	0.0054
BP	Free cholesterol in medium VLDL	27005778	metabolite	European	0.0945	0.0672	1.4053	0.1599	0.1213	0.0349	0.9905	0.0075	0.0052	0.0052
BP	Asthma	17611496	autoimmu	European	0.0848	0.0617	1.3749	1.69E-01	1.13E-01	0.0292	1.0124	0.0091	0.0116	0.0063

BP	Phospholipids in very small VLDL	27005778	metabolite	European	0.1078	0.0786	1.3706	0.1705	0.0901	0.0407	1.0146	0.0163	-0.0035	0.0059
BP	Concentration of medium HDL partic	27005778	metabolite	European	-0.1122	0.0823	-1.3632	0.1728	7.01E-02	0.0258	0.9935	0.0082	3.10E-03	0.0055
BP	Cholesterol esters in medium VLDL	27005778	metabolite	European	0.0823	0.0617	1.3332	1.83E-01	0.1591	0.0403	0.9831	0.0085	0.0014	0.0051
BP	Bipolar disorder	21926972	psychiatric	European	-0.0538	0.0404	-1.3292	1.84E-01	0.4435	0.0391	1.02	0.008	-5.00E-04	0.0053
BP	Total cholesterol in medium LDL	27005778	metabolite	European	0.1315	0.1002	1.3121	0.1895	0.0677	0.0519	1.0165	0.0257	-0.0062	0.0061
BP	Anorexia Nervosa	24514567	psychiatric	European	-0.0485	0.037	-1.3082	1.91E-01	0.5186	0.0309	0.9095	0.0076	3.00E-04	0.006
BP	Free cholesterol in very large HDL	27005778	metabolite	European	-0.1396	0.1102	-1.2675	0.205	0.0445	0.024	1.014	0.014	-0.0024	0.0054
BP	Crohns disease	26192919	autoimmu	European	0.047	0.0373	1.2595	0.2079	0.5143	0.0588	1.0195	0.0112	0.0018	0.0054
BP	Total cholesterol in large VLDL	27005778	metabolite	European	0.0839	0.0672	1.2486	0.2118	0.1222	0.0305	0.9889	0.007	0.0038	0.0055
BP	Total cholesterol in LDL	27005778	metabolite	European	0.1291	0.1039	1.2429	0.2139	0.0665	0.0564	1.0182	0.0279	-0.0053	0.0063
BP	Femoral neck bone mineral density	22504420	bone	Mixed	0.0435	0.0351	1.2381	0.2157	0.3046	0.0242	0.9788	0.0081	-8.00E-04	0.0056
BP	Total lipids in small LDL	27005778	metabolite	European	0.104	0.0864	1.2042	0.2285	0.0878	0.0492	1.0093	0.0199	-0.0035	0.0057
BP	Concentration of small LDL particles	27005778	metabolite	European	0.0964	0.0802	1.2015	0.2296	0.0977	0.0463	1.0072	0.0177	-0.0026	0.0056
BP	Concentration of very small VLDL par	27005778	metabolite	European	0.0792	0.0662	1.196	0.2317	0.1262	0.0388	1.0018	0.0119	3.00E-04	0.0054
BP	Phospholipids in medium LDL	27005778	metabolite	European	0.1052	0.088	1.1952	0.232	7.45E-02	0.0458	1.0103	0.0218	-3.00E-03	0.0058
BP	Apolipoprotein B	27005778	metabolite	European	0.1015	0.0857	1.1842	2.36E-01	0.089	0.0439	1.0081	0.0167	-5.00E-04	0.0059
BP	Apolipoprotein A-I	27005778	metabolite	European	-0.1047	0.09	-1.1637	2.45E-01	0.0752	0.0323	1.004	0.0125	7.00E-04	0.0056
BP	Concentration of IDL particles	27005778	metabolite	European	0.1025	0.0886	1.1567	0.2474	7.58E-02	0.0469	1.0202	0.02	-0.0022	0.006
BP	Sitting height ratio	25865494	anthropom	European	0.0622	0.0544	1.1449	0.2522	0.2284	0.0289	0.9784	0.0078	0.001	0.0063
BP	Mean diameter for HDL particles	27005778	metabolite	European	-0.0819	0.0722	-1.1349	0.2564	0.1103	0.0295	1.01	0.0189	-0.0041	0.0055
BP	Phospholipids in large LDL	27005778	metabolite	European	0.1131	0.1002	1.1287	0.259	0.0601	0.0491	1.0215	0.0249	-0.0037	0.0063
BP	Total cholesterol in medium VLDL	27005778	metabolite	European	0.0742	0.0659	1.1263	0.26	0.1322	0.0369	0.9881	0.0081	0.0044	0.0053
BP	Concentration of medium LDL particl	27005778	metabolite	European	0.1027	0.0918	1.1192	0.2631	0.08	0.0537	1.014	0.0232	-0.0039	0.0059
BP	Multiple sclerosis	21833088	autoimmu	European	0.1105	0.0992	1.114	0.2653	0.0521	0.0285	1.0656	0.0099	0.002	0.006
BP	Neo-consciousness	21173776	personality	European	-0.1164	0.1058	-1.0997	0.2715	0.0679	0.031	1.0023	0.0075	0.0015	0.0069
BP	Serum cystatin c	26831199	kidney	Mixed	-0.0525	0.048	-1.093	0.2744	0.1632	0.0696	0.9674	0.0146	-0.0088	0.0059
BP	Concentration of large LDL particles	27005778	metabolite	European	0.1027	0.0953	1.0777	0.2812	0.0736	0.0562	1.0195	0.025	-3.90E-03	0.0061
BP	Mean Caudate	25607358	brain_volu	European	0.0607	0.0569	1.0666	0.2862	0.2468	0.04	0.9685	0.0065	-0.0029	0.0052
BP	Triglycerides in chylomicrons and larg	27005778	metabolite	European	0.0796	0.0747	1.0661	0.2864	9.42E-02	0.0288	0.9891	0.0073	0.0067	0.0054
BP	Eczema	26482879	autoimmu	Mixed	0.0672	0.0634	1.0608	0.2888	0.0666	0.0158	1.0252	0.0076	5.00E-04	0.0052
BP	Total cholesterol in large LDL	27005778	metabolite	European	0.1074	0.1013	1.0603	0.289	0.0607	0.052	1.0205	0.0267	-0.0055	0.0063
BP	Systemic lupus erythematosus	26502338	autoimmu	European	0.0474	0.0449	1.0567	0.2907	0.3741	0.0612	1.1101	0.0105	4.00E-04	0.0059
BP	Cholesterol esters in medium LDL	27005778	metabolite	European	0.0947	0.091	1.041	2.98E-01	0.0795	0.0555	1.0134	0.0244	-0.0049	0.0059
BP	Phospholipids in very large HDL	27005778	metabolite	European	-0.0836	0.0803	-1.0401	0.2983	0.0867	0.0296	1.0076	0.0169	-0.0039	0.0054
BP	Triglycerides in very large HDL	27005778	metabolite	European	0.0781	0.0754	1.0362	0.3001	0.0851	0.0256	1.0115	0.0252	-0.0021	0.0053
BP	Concentration of medium VLDL parti	27005778	metabolite	European	0.0632	0.0612	1.0324	0.3019	0.1583	0.0379	0.9769	0.0079	0.0071	0.0054
BP	Total lipids in very small VLDL	27005778	metabolite	European	0.0722	0.07	1.0315	0.3023	0.1151	0.0385	1.0072	0.0124	4.00E-04	0.0055
BP	Phospholipids in very large VLDL	27005778	metabolite	European	0.0705	0.0685	1.03	0.303	0.109	0.0286	0.9838	0.007	0.0065	0.0055
BP	Phospholipids in IDL	27005778	metabolite	European	0.1002	0.0979	1.0239	0.3059	0.059	0.0459	1.0245	0.0221	-0.001	0.0062
BP	Mean Accumbens	25607358	brain_volu	European	0.0966	0.0945	1.0214	0.3071	0.0895	0.0371	0.9788	0.0068	-0.007	0.0053
BP	Total lipids in medium LDL	27005778	metabolite	European	0.0911	0.0899	1.0142	0.3105	8.10E-02	0.0552	1.0126	0.0241	-3.90E-03	0.006
BP	Free cholesterol in large VLDL	27005778	metabolite	European	0.0647	0.0641	1.0102	0.3124	0.1287	0.0303	0.9859	0.0069	5.80E-03	0.0055
BP	Free cholesterol in large LDL	27005778	metabolite	European	0.1022	0.1016	1.0065	0.3142	0.0583	0.0544	1.023	0.028	-0.0049	0.0065
BP	Total lipids in IDL	27005778	metabolite	European	0.0899	0.0903	0.9956	0.3194	0.0724	0.0491	1.022	0.0213	-0.0026	0.006

BP	Concentration of chylomicrons and la	27005778	metabolite	European	0.0603	0.0609	0.99	0.3222	0.1189	0.0271	0.9867	0.0066	0.0072	0.0053
BP	Citrate	27005778	metabolite	European	-0.0708	0.0716	-0.9883	0.323	7.09E-02	0.0211	1.0126	0.0084	-0.0023	0.0051
BP	Mean Pallidum	25607358	brain_volu	European	0.0712	0.073	0.976	0.3291	0.1761	0.0419	0.975	0.0077	0.001	0.0061
BP	Mean diameter for VLDL particles	27005778	metabolite	European	0.0625	0.0641	0.9751	0.3295	0.1314	0.0355	0.991	0.0087	0.0075	0.0057
BP	Phospholipids in small VLDL	27005778	metabolite	European	0.0651	0.067	0.973	0.3306	0.1246	0.0369	0.9953	0.0092	3.00E-03	0.0053
BP	Total lipids in large LDL	27005778	metabolite	European	0.0922	0.095	0.9706	0.3317	7.22E-02	0.0578	1.0188	0.0258	-0.004	0.0061
BP	Free cholesterol in IDL	27005778	metabolite	European	0.0894	0.0925	0.9667	0.3337	0.0646	0.0473	1.0256	0.0233	-0.0028	0.0064
BP	Total lipids in small HDL	27005778	metabolite	European	-0.0869	0.0903	-0.9634	0.3353	0.0591	0.0258	1	0.0074	0.0025	0.0052
BP	Glycoprotein acetyls; mainly a1-acid	27005778	metabolite	European	0.0622	0.065	0.9558	0.3392	1.12E-01	0.0285	0.9813	0.0069	0.0069	0.0053
BP	Leucine	27005778	metabolite	European	0.0989	0.107	0.9244	0.3553	0.0446	0.0211	1.0112	0.0069	-4.00E-04	0.0057
BP	Phospholipids in chylomicrons and la	27005778	metabolite	European	0.0663	0.0728	0.9109	0.3624	0.1007	0.0275	0.983	0.0073	0.0059	0.0056
BP	Total lipids in very large VLDL	27005778	metabolite	European	0.0552	0.0607	0.9106	0.3625	0.1424	0.0305	0.976	0.0075	0.0054	0.0054
BP	Forearm Bone mineral density	26367794	bone	Mixed	0.0966	0.1068	0.9039	0.3661	0.0783	0.0459	1.0136	0.0069	-0.0015	0.0056
BP	Triglycerides in very large VLDL	27005778	metabolite	European	0.0589	0.0656	0.8977	0.3693	0.1225	0.0292	0.9792	0.0069	7.40E-03	0.0056
BP	Concentration of very large VLDL par	27005778	metabolite	European	0.0572	0.065	0.8804	0.3787	0.1286	0.0318	0.9821	0.0074	7.10E-03	0.0055
BP	Total cholesterol in small LDL	27005778	metabolite	European	0.08	0.0924	0.8656	0.3867	0.0697	0.0492	1.0185	0.0222	-0.0026	0.0059
BP	Cholesterol esters in large LDL	27005778	metabolite	European	0.0763	0.093	0.8204	4.12E-01	0.0727	0.0573	1.017	0.0256	-0.0042	0.006
BP	Total cholesterol in very large HDL	27005778	metabolite	European	-0.105	0.1281	-0.8193	0.4126	0.031	0.023	1.0128	0.0118	-0.0028	0.0052
BP	Total lipids in chylomicrons and large	27005778	metabolite	European	0.0524	0.0649	0.8078	0.4192	0.1286	0.0285	0.9862	0.0073	7.30E-03	0.0054
BP	Glucose	27005778	metabolite	European	-0.059	0.0735	-0.8028	0.4221	0.0862	0.0217	0.9967	0.0074	0.0068	0.006
BP	Concentration of very large HDL parti	27005778	metabolite	European	-0.0738	0.092	-0.8021	0.4225	0.0618	0.0269	1.0009	0.0152	-0.0013	0.0053
BP	Primary biliary cirrhosis	26394269	autoimmu	European	0.0453	0.0569	0.7968	0.4256	0.3971	0.0628	1.0022	0.0099	1.31E-02	0.0066
BP	Total cholesterol in small VLDL	27005778	metabolite	European	0.0598	0.0762	0.7849	0.4325	0.0929	0.0346	1.0062	0.0106	8.00E-04	0.0055
BP	Creatinine	27005778	metabolite	European	-0.0447	0.0571	-0.7832	0.4335	1.15E-01	0.0254	1.0138	0.0076	-0.002	0.0058
BP	Transferrin	25352340	metal	European	0.0515	0.0661	0.7796	0.4356	0.1699	0.0801	1.061	0.0258	-0.0147	0.0072
BP	Inflammatory Bowel Disease (Euro)	26192919	autoimmu	European	0.0284	0.0368	0.7704	0.4411	0.3427	0.0343	1.0467	0.011	0.0029	0.0057
BP	Free cholesterol to esterified choles	27005778	metabolite	European	0.1008	0.1322	0.7629	0.4455	0.0558	0.0531	1.0141	0.0126	-0.0073	0.0058
BP	Urinary albumin-to-creatinine ratio	26631737	kidney	European	0.0489	0.0691	0.7082	0.4789	0.0446	0.0094	0.9969	0.0072	-0.0024	0.0057
BP	Mean Hippocampus	25607358	brain_volu	European	-0.0555	0.079	-0.703	0.482	0.1311	0.0402	0.9919	0.0075	6.00E-04	0.0059
BP	Total cholesterol in IDL	27005778	metabolite	European	0.0652	0.0935	0.697	0.4858	0.066	0.052	1.0237	0.0229	-0.0034	0.0061
BP	Mean platelet volume	22139419	haemotold	European	0.0287	0.0463	0.6198	0.5354	0.3267	0.0543	0.9791	0.0107	-4.20E-03	0.0063
BP	Total lipids in very large HDL	27005778	metabolite	European	-0.061	0.1043	-0.5844	0.559	5.28E-02	0.0278	1.0165	0.015	-0.0037	0.0054
BP	Serum creatinine (non-diabetes)	26831199	kidney	Mixed	-0.019	0.0343	-0.5556	0.5785	0.1176	0.0116	0.9733	0.0137	0.0038	0.0064
BP	Parkinsons disease	19915575	neurologic	European	0.0288	0.053	0.544	0.5864	0.4113	0.1193	1.1214	0.0103	-0.0056	0.0056
BP	Leptin_adjBMI	26833098	hormone	European	-0.0283	0.0548	-0.5162	0.6057	0.1006	0.0174	1.0008	0.0072	0.0041	0.0057
BP	Platelet count	22139419	haemotold	European	0.018	0.0354	0.508	0.6115	0.1189	0.0116	0.9865	0.0081	0.0066	0.005
BP	Femoral Neck bone mineral density	26367794	bone	Mixed	-0.0195	0.0402	-0.4833	0.6289	0.1194	0.0143	0.9796	0.0082	0.0033	0.0056
BP	Serum creatinine	26831199	kidney	Mixed	-0.0161	0.0344	-0.4679	0.6399	0.1089	0.0101	0.973	0.0139	0.004	0.0068
BP	Difference in height between adolesc	23449627	anthropom	European	-0.0279	0.0688	-0.4063	0.6845	0.4424	0.1123	0.9823	0.007	-6.00E-04	0.0052
BP	Adiponectin	22479202	cardiomet	Mixed	-0.0238	0.0609	-0.3909	6.96E-01	0.1146	0.0273	1.0238	0.0138	-0.0047	0.0059
BP	Forced expiratory volume in 1 second	28166213	lung_funct	European	-0.0139	0.0361	-0.3837	0.7012	0.2606	0.0212	0.9719	0.0093	4.00E-04	0.0064
BP	Fasting proinsulin	20081858	glycemic	European	0.0311	0.0825	0.3774	0.7059	1.96E-01	0.0882	0.9802	0.0104	0.0077	0.0061
BP	Alanine	27005778	metabolite	European	-0.0226	0.0668	-0.3388	7.35E-01	9.38E-02	0.0282	1.0075	0.0075	1.90E-03	0.0056
BP	Height; Females at age 10 and males	23449627	anthropom	European	-0.0148	0.046	-0.3222	0.7473	0.4352	0.0468	0.951	0.0086	0.0105	0.0061

A) 1e-5 GP

Supplementary Table 7A: Gene prioritisation with DEPICT (input SNPs with p<1e-5)

Locus	Nr of genes in locus	Chromosome and position	GWAS P value	Ensembl gene ID	Gene symbol	Nominal P value	Gene closest to lead SNP	Nature Genetics (2014)	Top cis eQTL SNP (Westra et al.)	False discovery rate
rs9804988	1	chr12:236	1.31E-16	ENSG0000	SOX5	6.69E-05	TRUE	-	<0.05	
rs7660676	1	chr4:6206	5.24E-06	ENSG0000	LPHN3	1.35E-04	TRUE	-	<0.05	
rs599550	1	chr18:528	6.25E-07	ENSG0000	TCF4	2.44E-04	TRUE	rs1660233	<0.05	
rs2383521	1	chr14:334	3.97E-07	ENSG0000	NPAS3	4.07E-04	TRUE	rs6571607	<0.05	
rs5587595	1	chr18:422	8.92E-06	ENSG0000	SETBP1	7.71E-04	TRUE	rs1036929	<0.05	
rs1940720	2	chr11:112	3.16E-08	ENSG0000	NCAM1	8.94E-04	FALSE	rs1711531	<0.05	
rs1173225	1	chr13:582	6.53E-07	ENSG0000	PCDH17	1.27E-03	TRUE	-	<0.05	
rs3795027	2	chr19:187	2.43E-06	ENSG0000	KLHL26	1.83E-03	FALSE	rs3795028	<0.05	
rs1087026	3	chr10:133	9.78E-09	ENSG0000	DPYSL4	2.18E-03	TRUE	rs2101613	<0.05	
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	PTCH2	2.51E-03	FALSE	rs4660821	<0.05	
rs2546944	1	chr5:1667	2.54E-06	ENSG0000	ODZ2	3.33E-03	FALSE	rs2243779	<0.05	
rs1617156	7	chr12:123	1.31E-07	ENSG0000	SETD8	3.40E-03	FALSE	rs1236687	<0.05	
rs3531883	3	chr19:463	1.21E-07	ENSG0000	IRF2BP1	3.43E-03	TRUE	-	<0.05	
rs1682797	1	chr3:1155	4.03E-06	ENSG0000	LSAMP	3.46E-03	TRUE	rs4831212	<0.05	
rs7734275	3	chr5:1109	8.31E-06	ENSG0000	C5orf13	3.70E-03	TRUE	-	<0.05	
rs1098343	1	chr9:1191	3.29E-07	ENSG0000	ASTN2	4.04E-03	FALSE	-	<0.05	
rs7147566	2	chr14:300	4.19E-06	ENSG0000	PRKD1	4.06E-03	TRUE	rs1014510	<0.05	
rs7323338	1	chr12:125	5.63E-06	ENSG0000	TMEM132	4.49E-03	TRUE	rs4765270	<0.05	
rs2076587	4	chr1:1122	8.75E-06	ENSG0000	KCND3	4.61E-03	FALSE	rs1348469	<0.05	
rs3795027	2	chr19:187	2.43E-06	ENSG0000	CRTC1	4.89E-03	TRUE	rs1166598	<0.05	
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	BSN	5.06E-03	FALSE	-	<0.05	
rs13169	2	chr19:797	7.89E-08	ENSG0000	MIR3187	5.40E-03	FALSE	-	<0.05	
rs7613469	1	chr13:863	2.93E-08	ENSG0000	SLITRK6	5.62E-03	TRUE	-	<0.05	
rs6188430	15	chr11:462	6.44E-06	ENSG0000	LRP4	5.85E-03	FALSE	-	<0.05	
rs3453126	1	chr11:132	6.84E-06	ENSG0000	OPCML	6.57E-03	TRUE	rs2509236	<0.05	
rs6018311	1	chr10:555	9.20E-06	ENSG0000	PCDH15	6.61E-03	TRUE	rs1076303	<0.05	
rs8079725	1	chr17:793	1.16E-06	ENSG0000	BAHCC1	7.86E-03	TRUE	-	<0.05	
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	ZSWIM5	8.12E-03	TRUE	-	<0.05	
rs509345	7	chr1:1502	4.39E-06	ENSG0000	RPRD2	8.20E-03	FALSE	rs1211925	<0.05	
rs867636	1	chr3:1140	3.24E-06	ENSG0000	ZBTB20	8.23E-03	FALSE	rs1767048	<0.05	
rs3531883	3	chr19:463	1.21E-07	ENSG0000	MYPOP	8.67E-03	FALSE	-	<0.05	
rs1107648	1	chr16:495	1.07E-06	ENSG0000	ZNF423	9.04E-03	TRUE	-	<0.05	
rs1921117	1	chr5:3119	9.86E-09	ENSG0000	CDH6	9.10E-03	TRUE	rs7722943	<0.05	
rs1462620	1	chr5:6751	7.85E-06	ENSG0000	PIK3R1	9.21E-03	TRUE	rs1689746	<0.05	
rs2219837	1	chr10:737	2.51E-12	ENSG0000	CHST3	9.28E-03	TRUE	-	<0.05	
rs1740032	2	chr2:1784	1.11E-06	ENSG0000	PDE11A	9.37E-03	FALSE	-	<0.05	
rs3511738	3	chr19:558	1.65E-06	ENSG0000	FAM71E2	9.47E-03	FALSE	rs8113016	<0.05	

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rs818215	1	chr3:8500	3.86E-07	ENSG0000	CADM2	0.01	TRUE	rs9811546	<0.05
rs1162783	2	chr14:420	1.02E-07	ENSG0000	LRFN5	0.01	TRUE	-	<0.20
rs1419294	1	chr2:1756	5.14E-06	ENSG0000	CHN1	0.01	TRUE	rs6751261	<0.20
rs2076587	4	chr1:1122	8.75E-06	ENSG0000	C1orf183	0.02	FALSE	rs7548973	<0.20
rs7733819	1	chr18:601	9.72E-06	ENSG0000	ZCCHC2	0.02	TRUE	rs1087179	<0.20
rs6932028	1	chr6:8539	3.10E-06	ENSG0000	TBX18	0.02	TRUE	-	<0.20
rs706931	3	chr6:1109	6.41E-06	ENSG0000	CDK19	0.02	TRUE	rs2136677	<0.20
rs7952320	1	chr11:824	4.44E-06	ENSG0000	LMO1	0.02	TRUE	-	<0.20
rs7688279	1	chr7:5346	6.56E-08	ENSG0000	TNRC18	0.03	FALSE	rs852374	<0.20
rs2910576	1	chr5:5774	1.97E-07	ENSG0000	PLK2	0.03	TRUE	rs1051314	<0.20
rs1204765	1	chr20:496	1.91E-08	ENSG0000	KCNG1	0.03	TRUE	rs4809820	<0.20
rs1162783	2	chr14:420	1.02E-07	ENSG0000	-	0.03	FALSE	-	<0.20
rs3415998	2	chr19:460	1.13E-06	ENSG0000	GPR4	0.03	TRUE	-	<0.20
rs7316114	6	chr12:122	7.94E-06	ENSG0000	RSRC2	0.03	FALSE	rs1473553	<0.20
rs1281434	3	chr12:465	3.91E-06	ENSG0000	SLC38A2	0.04	TRUE	rs4768697	<0.20
rs4498521	2	chr8:1415	9.28E-07	ENSG0000	PTK2	0.04	FALSE	rs7011412	<0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	ZCCHC11	0.04	TRUE	rs1710724	<0.20
rs7302816	1	chr12:899	1.06E-07	ENSG0000	ATP2B1	0.04	FALSE	rs1701686	<0.20
rs2284569	1	chr21:350	1.73E-06	ENSG0000	ITSN1	0.05	FALSE	rs2251854	<0.20
rs7226995	1	chr18:498	9.86E-09	ENSG0000	DCC	0.05	FALSE	-	<0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	ZNF408	0.05	TRUE	-	>0.20
rs265361	1	chr6:1292	1.24E-07	ENSG0000	LAMA2	0.05	FALSE	rs7760943	>0.20
rs9930051	1	chr16:826	9.21E-07	ENSG0000	CDH13	0.05	FALSE	rs1696225	>0.20
rs9529217	1	chr13:668	2.54E-06	ENSG0000	PCDH9	0.06	TRUE	rs9564360	>0.20
rs1050817	1	chr13:107	6.97E-06	ENSG0000	EFNB2	0.06	TRUE	rs9514545	>0.20
rs2856811	1	chr1:1158	9.05E-07	ENSG0000	NGF	0.06	TRUE	rs2268793	>0.20
rs9292468	1	chr5:3268	3.18E-07	ENSG0000	NPR3	0.06	TRUE	-	>0.20
rs1361754	4	chr1:2056	1.67E-06	ENSG0000	NUCKS1	0.06	FALSE	rs1772148	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG0000	-	0.07	FALSE	-	>0.20
rs6204002	1	chr16:175	5.03E-06	ENSG0000	MAPK8IP3	0.07	TRUE	rs1028590	>0.20
rs1142295	1	chr2:1409	8.94E-06	ENSG0000	LRP1B	0.07	TRUE	rs1223322	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	CHRM4	0.07	FALSE	-	>0.20
rs4974563	2	chr4:1145	2.44E-08	ENSG0000	-	0.07	TRUE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	PAC SIN3	0.08	FALSE	-	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	ZNF821	0.08	FALSE	-	>0.20
rs1751313	4	chr1:3954	3.07E-06	ENSG0000	MACF1	0.08	FALSE	rs645061;	>0.20
rs7788052	1	chr7:3341	1.19E-07	ENSG0000	SDK1	0.08	TRUE	-	>0.20
rs4909605	1	chr8:1354	3.25E-06	ENSG0000	ZFAT	0.09	TRUE	rs1178063	>0.20
rs1343766	1	chr7:9748	6.14E-06	ENSG0000	ASNS	0.09	TRUE	rs1198317	>0.20
rs7236305	1	chr18:670	1.14E-06	ENSG0000	DOK6	0.09	TRUE	rs1115151	>0.20
rs4498521	2	chr8:1415	9.28E-07	ENSG0000	EIF2C2	0.1	TRUE	rs2977461	>0.20
rs1296948	1	chr18:348	1.06E-06	ENSG0000	CELF4	0.1	TRUE	-	>0.20
rs1047597	1	chr5:1708	5.34E-09	ENSG0000	FGF18	0.11	TRUE	rs919325	>0.20
rs1001830	1	chr4:8874	2.72E-06	ENSG0000	MEPE	0.11	TRUE	-	>0.20
rs1617156	7	chr12:123	1.31E-07	ENSG0000	PITPNM2	0.11	TRUE	-	>0.20
rs1617156	7	chr12:123	1.31E-07	ENSG0000	SBNO1	0.12	FALSE	rs1790116	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	AMBRA1	0.12	FALSE	-	>0.20

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rs623738	1	chr3:1072	4.02E-06	ENSG0000	BBX	0.12	TRUE	rs9862385	>0.20
rs1131739	1	chr4:4603	8.17E-06	ENSG0000	GABRG1	0.12	TRUE	-	>0.20
rs1142700	1	chr4:5424	7.11E-06	ENSG0000	FIP1L1	0.13	FALSE	rs2616422	>0.20
rs8045567	1	chr16:889	7.02E-08	ENSG0000	CBFA2T3	0.13	TRUE	rs3934812	>0.20
rs2861375	1	chr15:673	6.72E-06	ENSG0000	SMAD3	0.13	TRUE	rs1244327	>0.20
rs4907768	1	chr13:112	5.61E-06	ENSG0000	LINC00354	0.13	TRUE	-	>0.20
rs706931	3	chr6:1109	6.41E-06	ENSG0000	AMD1	0.14	FALSE	rs1279578	>0.20
rs1191524	1	chr3:6811	7.63E-07	ENSG0000	GRM7	0.14	TRUE	rs161455	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG0000	SLC25A21	0.14	FALSE	rs848087	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG0000	TTC6	0.14	FALSE	-	>0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	ZFYVE9	0.15	FALSE	-	>0.20
rs7317437	1	chr3:1688	7.86E-07	ENSG0000	MECOM	0.15	TRUE	-	>0.20
rs1693182	1	chr12:175	2.49E-06	ENSG0000	IQSEC3	0.15	TRUE	rs2291926	>0.20
rs2076587	4	chr1:1122	8.75E-06	ENSG0000	DDX20	0.16	FALSE	rs1181112	>0.20
rs6495162	1	chr15:754	6.44E-06	ENSG0000	C15orf39	0.16	TRUE	rs8040061	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	DAG1	0.16	FALSE	rs6784820	>0.20
rs1761935	6	chr2:6334	3.36E-07	ENSG0000	DBIL5P2	0.16	FALSE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	RHOA	0.17	TRUE	-	>0.20
rs8013931	1	chr14:631	3.18E-07	ENSG0000	KCNH5	0.17	TRUE	rs1289006	>0.20
rs1800248	1	chr7:9402	3.00E-06	ENSG0000	COL1A2	0.18	TRUE	rs400218	>0.20
rs1174378	1	chr8:1394	3.53E-06	ENSG0000	SGCZ	0.18	FALSE	-	>0.20
rs1126455	6	chr1:1566	5.29E-07	ENSG0000	PRCC	0.19	FALSE	-	>0.20
rs1617156	7	chr12:123	1.31E-07	ENSG0000	ABCB9	0.19	FALSE	rs1615350	>0.20
rs6536404	1	chr4:1600	2.52E-06	ENSG0000	RAPGEF2	0.19	TRUE	-	>0.20
rs1010539	1	chr8:1132	8.21E-06	ENSG0000	CSMD3	0.19	TRUE	-	>0.20
rs4508867	1	chr4:2451	4.17E-06	ENSG0000	DHX15	0.2	TRUE	rs4321620	>0.20
rs6228356	3	chr3:1403	8.61E-06	ENSG0000	SPSB4	0.2	TRUE	-	>0.20
rs1761935	6	chr2:6334	3.36E-07	ENSG0000	PELI1	0.2	FALSE	rs869738	>0.20
rs1272105	4	chr19:453	3.83E-06	ENSG0000	APOE	0.2	FALSE	-	>0.20
rs3788337	2	chr22:234	5.54E-06	ENSG0000	GNAZ	0.2	TRUE	-	>0.20
rs7734275	3	chr5:1109	8.31E-06	ENSG0000	EPB41L4A	0.2	FALSE	-	>0.20
rs1126455	6	chr1:1566	5.29E-07	ENSG0000	HDGF	0.21	TRUE	rs2150906	>0.20
rs7316114	6	chr12:122	7.94E-06	ENSG0000	ZCCHC8	0.21	TRUE	-	>0.20
rs6978112	2	chr7:1855	3.16E-06	ENSG0000	-	0.22	TRUE	-	>0.20
rs1087026	3	chr10:133	9.78E-09	ENSG0000	STK32C	0.22	FALSE	rs7099831	>0.20
rs7316114	6	chr12:122	7.94E-06	ENSG0000	-	0.23	FALSE	-	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG0000	FOXA1	0.23	FALSE	-	>0.20
rs1361754	4	chr1:2056	1.67E-06	ENSG0000	SLC41A1	0.23	FALSE	rs823080	>0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	GPX7	0.24	FALSE	rs835339	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	MUTYH	0.25	FALSE	rs1213936	>0.20
rs6037486	2	chr20:308	4.50E-06	ENSG0000	UBOX5	0.25	FALSE	rs306757;	>0.20
rs3445410	1	chr20:515	2.08E-06	ENSG0000	TSHZ2	0.26	TRUE	-	>0.20
rs7665749	1	chr1:4339	6.64E-06	ENSG0000	SLC2A1	0.26	TRUE	rs1770803	>0.20
rs3511738	3	chr19:558	1.65E-06	ENSG0000	IL11	0.26	FALSE	-	>0.20
rs1120372	1	chr2:2089	1.45E-06	ENSG0000	-	0.26	TRUE	-	>0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	PRPF38A	0.27	FALSE	-	>0.20
rs1940720	2	chr11:112	3.16E-08	ENSG0000	-	0.28	TRUE	-	>0.20

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rs1909544	1	chr5:1355	2.40E-07	ENSG0000	TRPC7	0.28	TRUE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	DGKZ	0.28	FALSE	rs4625425	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	RNF123	0.29	FALSE	-	>0.20
rs1453867	1	chr2:2328	1.93E-07	ENSG0000	DIS3L2	0.29	TRUE	rs6743962	>0.20
rs2672596	1	chr10:124	4.06E-11	ENSG0000	HTRA1	0.3	TRUE	rs2292627	>0.20
rs509345	7	chr1:1502	4.39E-06	ENSG0000	PRPF3	0.3	FALSE	rs1050818	>0.20
rs1751313	4	chr1:3954	3.07E-06	ENSG0000	BMP8A	0.31	FALSE	-	>0.20
rs1084948	6	chr12:656	4.09E-07	ENSG0000	GAPDH	0.31	TRUE	rs1230302	>0.20
rs13169	2	chr19:797	7.89E-08	ENSG0000	PTBP1	0.31	TRUE	rs4375794	>0.20
rs509345	7	chr1:1502	4.39E-06	ENSG0000	MRPS21	0.31	TRUE	-	>0.20
rs1751313	4	chr1:3954	3.07E-06	ENSG0000	-	0.32	TRUE	-	>0.20
rs7467334	1	chr9:1214	3.90E-06	ENSG0000	-	0.33	TRUE	-	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	TOE1	0.33	FALSE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	CKAP5	0.34	FALSE	-	>0.20
rs1841497	1	chr1:7186	4.92E-06	ENSG0000	NEGR1	0.34	TRUE	-	>0.20
rs1084948	6	chr12:656	4.09E-07	ENSG0000	NCAPD2	0.35	FALSE	rs1106423	>0.20
rs1084948	6	chr12:656	4.09E-07	ENSG0000	IFFO1	0.35	FALSE	rs1084948	>0.20
rs509345	7	chr1:1502	4.39E-06	ENSG0000	C1orf51	0.35	FALSE	-	>0.20
rs1311401	5	chr4:2845	2.06E-06	ENSG0000	ADD1	0.36	FALSE	rs1684358	>0.20
rs1709219	5	chr20:335	1.94E-07	ENSG0000	MYH7B	0.37	TRUE	-	>0.20
rs1379837	2	chr2:2112	4.72E-07	ENSG0000	LANCL1	0.37	FALSE	rs3856348	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	ATXN1L	0.38	FALSE	-	>0.20
rs1215542	1	chr7:1401	5.27E-08	ENSG0000	MKRN1	0.38	TRUE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	C11orf49	0.38	FALSE	rs4494268	>0.20
rs6228356	3	chr3:1403	8.61E-06	ENSG0000	TRIM42	0.38	FALSE	-	>0.20
rs3604723	1	chr15:538	2.95E-06	ENSG0000	WDR72	0.39	TRUE	rs2126188	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	ARFGAP2	0.4	FALSE	rs4647709	>0.20
rs3531883	3	chr19:463	1.21E-07	ENSG0000	NANOS2	0.4	FALSE	-	>0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	FAM159A	0.4	FALSE	rs1158121	>0.20
rs7266676	1	chr8:6924	5.77E-14	ENSG0000	C8orf34	0.4	FALSE	-	>0.20
rs1709219	5	chr20:335	1.94E-07	ENSG0000	TRPC4AP	0.41	FALSE	rs6120819	>0.20
rs1245301	1	chr17:497	3.76E-07	ENSG0000	CA10	0.42	TRUE	rs6504736	>0.20
rs6073575	2	chr20:435	9.54E-06	ENSG0000	TOMM34	0.42	TRUE	rs2180292	>0.20
rs1379837	2	chr2:2112	4.72E-07	ENSG0000	CPS1	0.42	FALSE	-	>0.20
rs1281434	3	chr12:465	3.91E-06	ENSG0000	SLC38A1	0.43	FALSE	rs1118338	>0.20
rs6037486	2	chr20:308	4.50E-06	ENSG0000	FASTKD5	0.43	FALSE	rs2422859	>0.20
rs1591789	1	chr9:1033	3.37E-06	ENSG0000	MURC	0.44	TRUE	-	>0.20
rs1311401	5	chr4:2845	2.06E-06	ENSG0000	NOP14	0.44	TRUE	-	>0.20
rs416223	1	chr5:1044	1.32E-06	ENSG0000	RAB9BP1	0.44	TRUE	-	>0.20
rs509345	7	chr1:1502	4.39E-06	ENSG0000	ECM1	0.44	FALSE	-	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	HPDL	0.45	FALSE	-	>0.20
rs6745423	1	chr2:5865	5.94E-06	ENSG0000	-	0.45	TRUE	-	>0.20
rs1087026	3	chr10:133	9.78E-09	ENSG0000	JAKMIP3	0.46	FALSE	rs1114624	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	KIF2C	0.46	FALSE	-	>0.20
rs6137071	1	chr2:1059	5.21E-06	ENSG0000	FHL2	0.47	FALSE	rs1019018	>0.20
rs1272105	4	chr19:453	3.83E-06	ENSG0000	TOMM40	0.48	FALSE	-	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	PLK3	0.48	FALSE	-	>0.20

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rs9998332	2	chr4:1596	4.99E-07	ENSG0000	C4orf45	0.48	TRUE	-	>0.20
rs1751313	4	chr1:3954	3.07E-06	ENSG0000	KIAA0754	0.48	FALSE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	CREB3L1	0.49	FALSE	-	>0.20
rs1281434	3	chr12:465	3.91E-06	ENSG0000	-	0.49	FALSE	-	>0.20
rs1268085	2	chr8:9549	8.78E-09	ENSG0000	-	0.5	FALSE	-	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	UROD	0.5	FALSE	-	>0.20
rs4141466	2	chr1:7566	5.94E-06	ENSG0000	-	0.52	TRUE	-	>0.20
rs1268085	2	chr8:9549	8.78E-09	ENSG0000	KIAA1429	0.52	TRUE	-	>0.20
rs6207006	1	chr17:681	5.11E-06	ENSG0000	KCNJ2	0.53	TRUE	rs4968799	>0.20
rs747808	1	chr1:2157	6.40E-06	ENSG0000	USH2A	0.53	FALSE	rs3767255	>0.20
rs1890746	6	chr3:1529	3.48E-06	ENSG0000	SH3BP5	0.53	FALSE	rs826425	>0.20
rs509345	7	chr1:1502	4.39E-06	ENSG0000	TARS2	0.53	FALSE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	F2	0.54	FALSE	-	>0.20
rs2438639	2	chr5:7928	5.26E-06	ENSG0000	THBS4	0.54	FALSE	rs1565513	>0.20
rs7268545	1	chr1:1040	9.45E-06	ENSG0000	RNPC3	0.55	TRUE	-	>0.20
rs7316114	6	chr12:122	7.94E-06	ENSG0000	KNTC1	0.55	FALSE	rs7314410	>0.20
rs7734275	3	chr5:1109	8.31E-06	ENSG0000	EPB41L4A	0.55	FALSE	-	>0.20
rs1126455	6	chr1:1566	5.29E-07	ENSG0000	MRPL24	0.55	FALSE	-	>0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	ORC1	0.56	FALSE	-	>0.20
rs4898835	1	chr14:548	5.59E-06	ENSG0000	CDKN3	0.57	TRUE	-	>0.20
rs1311401	5	chr4:2845	2.06E-06	ENSG0000	C4orf10	0.59	FALSE	-	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	IST1	0.59	FALSE	-	>0.20
rs1084948	6	chr12:656	4.09E-07	ENSG0000	MRPL51	0.6	FALSE	rs1045546	>0.20
rs2438639	2	chr5:7928	5.26E-06	ENSG0000	-	0.62	TRUE	-	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	PHLPP2	0.62	FALSE	-	>0.20
rs7718889	1	chr5:7347	4.16E-06	ENSG0000	-	0.64	TRUE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	ATG13	0.65	FALSE	-	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	TAT	0.66	FALSE	-	>0.20
rs7011587	1	chr8:1926	9.00E-06	ENSG0000	CSGALNAC	0.67	FALSE	rs4481612	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	EIF2B3	0.68	FALSE	-	>0.20
rs2505982	7	chr1:5260	3.53E-07	ENSG0000	CC2D1B	0.68	FALSE	rs7513934	>0.20
rs1089278	1	chr11:121	9.98E-06	ENSG0000	BLID	0.69	TRUE	-	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	AP1G1	0.69	FALSE	rs1735631	>0.20
rs3788337	2	chr22:234	5.54E-06	ENSG0000	RTDR1	0.69	FALSE	rs6003527	>0.20
rs1167071	1	chr4:1351	2.45E-06	ENSG0000	-	0.7	TRUE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	DDB2	0.71	FALSE	rs3758674	>0.20
rs1311401	5	chr4:2845	2.06E-06	ENSG0000	MFSD10	0.72	FALSE	-	>0.20
rs1761935	6	chr2:6334	3.36E-07	ENSG0000	MDH1	0.72	TRUE	-	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	BTBD19	0.73	FALSE	-	>0.20
rs1761935	6	chr2:6334	3.36E-07	ENSG0000	VPS54	0.73	FALSE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	APEH	0.73	FALSE	rs3197999	>0.20
rs1272105	4	chr19:453	3.83E-06	ENSG0000	PVRL2	0.75	FALSE	rs1187958	>0.20
rs6228356	3	chr3:1403	8.61E-06	ENSG0000	SLC25A36	0.75	FALSE	-	>0.20
rs1272105	4	chr19:453	3.83E-06	ENSG0000	APOC1	0.76	TRUE	-	>0.20
rs1150768	1	chr9:1402	9.75E-09	ENSG0000	EXD3	0.76	TRUE	-	>0.20
rs706931	3	chr6:1109	6.41E-06	ENSG0000	RPF2	0.76	FALSE	-	>0.20
rs4141466	2	chr1:7566	5.94E-06	ENSG0000	SLC44A5	0.76	FALSE	-	>0.20

A) 1e-5 GP

rs6978112	2	chr7:1855	3.16E-06	ENSG0000	MAD1L1	0.77	FALSE	rs7783715	>0.20
rs6836166	1	chr4:1644	7.19E-06	ENSG0000	MARCH1	0.78	FALSE	rs719307;	>0.20
rs1890746	6	chr3:1529	3.48E-06	ENSG0000	COLQ	0.78	TRUE	rs6781355	>0.20
rs5957242	3	chr3:1992	9.18E-06	ENSG0000	PP2D1	0.79	FALSE	-	>0.20
rs509345	7	chr1:1502	4.39E-06	ENSG0000	C1orf54	0.79	FALSE	rs2274127	>0.20
rs1890746	6	chr3:1529	3.48E-06	ENSG0000	EAF1	0.8	FALSE	rs2455809	>0.20
rs7147566	2	chr14:300	4.19E-06	ENSG0000	-	0.8	FALSE	-	>0.20
rs1761935	6	chr2:6334	3.36E-07	ENSG0000	WDPCP	0.8	FALSE	-	>0.20
rs1617156	7	chr12:123	1.31E-07	ENSG0000	C12orf65	0.81	FALSE	-	>0.20
rs3511738	3	chr19:558	1.65E-06	ENSG0000	TMEM190	0.81	TRUE	rs7253685	>0.20
rs1177848	1	chr8:6651	4.44E-06	ENSG0000	ARMC1	0.81	TRUE	rs1008736	>0.20
rs3415998	2	chr19:460	1.13E-06	ENSG0000	OPA3	0.82	FALSE	rs1264226	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	NICN1	0.82	FALSE	rs3870339	>0.20
rs2076587	4	chr1:1122	8.75E-06	ENSG0000	-	0.83	TRUE	-	>0.20
rs6073575	2	chr20:435	9.54E-06	ENSG0000	PABPC1L	0.84	FALSE	-	>0.20
rs1709219	5	chr20:335	1.94E-07	ENSG0000	PROCR	0.85	FALSE	-	>0.20
rs1890746	6	chr3:1529	3.48E-06	ENSG0000	BTD	0.85	FALSE	rs2470530	>0.20
rs7316114	6	chr12:122	7.94E-06	ENSG0000	CLIP1	0.86	FALSE	-	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG0000	MIPOL1	0.86	TRUE	rs1884803	>0.20
rs1617156	7	chr12:123	1.31E-07	ENSG0000	MPHOSPH	0.86	FALSE	-	>0.20
rs5957242	3	chr3:1992	9.18E-06	ENSG0000	EFHB	0.86	TRUE	rs1112892	>0.20
rs1084948	6	chr12:656	4.09E-07	ENSG0000	VAMP1	0.87	FALSE	rs2534722	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	BEST4	0.87	FALSE	-	>0.20
rs1126455	6	chr1:1566	5.29E-07	ENSG0000	RRNAD1	0.88	FALSE	rs1240420	>0.20
rs1095648	1	chr8:1303	5.88E-15	ENSG0000	-	0.88	TRUE	-	>0.20
rs1084948	6	chr12:656	4.09E-07	ENSG0000	TAPBPL	0.88	FALSE	rs2244083	>0.20
rs7267886	1	chr4:1130	2.20E-06	ENSG0000	C4orf32	0.88	TRUE	rs4833392	>0.20
rs1126455	6	chr1:1566	5.29E-07	ENSG0000	NTRK1	0.88	FALSE	-	>0.20
rs7469357	1	chr2:6762	1.15E-06	ENSG0000	ETAA1	0.89	TRUE	-	>0.20
rs5957242	3	chr3:1992	9.18E-06	ENSG0000	RAB5A	0.89	FALSE	rs1307289	>0.20
rs4974563	2	chr4:1145	2.44E-08	ENSG0000	SPON2	0.89	FALSE	rs7684536	>0.20
rs1617156	7	chr12:123	1.31E-07	ENSG0000	RILPL2	0.89	FALSE	rs1662	>0.20
rs1361754	4	chr1:2056	1.67E-06	ENSG0000	PM20D1	0.9	TRUE	rs823074	>0.20
rs7681650	1	chr10:311	4.72E-06	ENSG0000	ZNF438	0.9	TRUE	rs2995654	>0.20
rs1890746	6	chr3:1529	3.48E-06	ENSG0000	METTL6	0.91	FALSE	-	>0.20
rs1311401	5	chr4:2845	2.06E-06	ENSG0000	GRK4	0.91	FALSE	rs2285084	>0.20
rs1126455	6	chr1:1566	5.29E-07	ENSG0000	SH2D2A	0.93	FALSE	rs1683762	>0.20
rs7316114	6	chr12:122	7.94E-06	ENSG0000	HCAR1	0.93	FALSE	-	>0.20
rs324300	1	chr11:296	4.80E-09	ENSG0000	-	0.93	TRUE	-	>0.20
rs1709219	5	chr20:335	1.94E-07	ENSG0000	GSS	0.94	FALSE	-	>0.20
rs1761935	6	chr2:6334	3.36E-07	ENSG0000	UGP2	0.94	FALSE	rs1016516	>0.20
rs1313509	2	chr4:1023	3.49E-08	ENSG0000	BANK1	0.94	FALSE	rs1703197	>0.20
rs1890746	6	chr3:1529	3.48E-06	ENSG0000	HAACL1	0.95	FALSE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	ARHGAP1	0.95	FALSE	rs2070852	>0.20
rs1313509	2	chr4:1023	3.49E-08	ENSG0000	SLC39A8	0.95	TRUE	rs7655493	>0.20
rs1740032	2	chr2:1784	1.11E-06	ENSG0000	-	0.95	TRUE	-	>0.20
rs1117955	1	chr11:123	1.98E-06	ENSG0000	TMEM225	0.96	TRUE	-	>0.20

A) 1e-5 GP

rs1417271	1	chr2:2141	8.95E-06	ENSG0000	SPAG16	0.96	FALSE	rs7558283	>0.20
rs3738620	1	chr1:2350	8.51E-06	ENSG0000	-	0.96	TRUE	-	>0.20
rs1700746	1	chr4:8471	6.56E-06	ENSG0000	-	0.96	FALSE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	AMT	0.96	FALSE	rs1568661	>0.20
rs1503697	12	chr1:4520	3.00E-06	ENSG0000	HECTD3	0.96	FALSE	-	>0.20
rs9998332	2	chr4:1596	4.99E-07	ENSG0000	FNIP2	0.97	FALSE	rs1311488	>0.20
rs1210486	1	chr2:5399	2.40E-06	ENSG0000	CHAC2	0.97	TRUE	-	>0.20
rs6202910	1	chr16:494	5.30E-06	ENSG0000	C16orf78	0.97	TRUE	-	>0.20
rs6188430	15	chr11:462	6.44E-06	ENSG0000	HARBI1	0.98	FALSE	-	>0.20
rs1017741	1	chr6:8115	7.28E-06	ENSG0000	-	0.99	TRUE	-	>0.20
rs6948241	1	chr7:1260	1.08E-06	ENSG0000	-	0.99	TRUE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	BSN-AS2	0.99	FALSE	-	>0.20
rs1361754	4	chr1:2056	1.67E-06	ENSG0000	RAB7L1	0.99	FALSE	rs823114	>0.20
rs4703253	1	chr5:1028	2.01E-08	ENSG0000	NUDT12	1	TRUE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG0000	TCTA	1	FALSE	rs9881860	>0.20
rs1709219	5	chr20:335	1.94E-07	ENSG0000	EDEM2	1	FALSE	rs6058194	>0.20
rs6205380	7	chr16:715	6.06E-07	ENSG0000	MARVELD	1	FALSE	-	>0.20

B) 1e-5 GSE

Supplementary Table 7B: Gene set enrichment analysis with DEPICT (input SNPs with p<1e-5, nominal)

Original gene set ID	Original gene set description	Nominal P value	False discovery rate	Reconstituted gene set Z score gene 1	Reconstituted gene set Z score gene 2
MP:0001469	abnormal contextual conditioning beh	3.24E-05	<0.20	GABRG1 (4.4)	OPCML (4.4)
MP:0001454	abnormal cued conditioning behavior	4.29E-05	<0.20	STK32C (3.3)	CHRM4 (3.3)
GO:0060284	regulation of cell development	7.80E-05	<0.20	NPAS3 (3.3)	ENSG000000000000
ENSG00000155974	GRIP1 PPI subnetwork	1.12E-04	<0.20	LRP1B (4.4)	CADM2 (4.4)
ENSG00000120251	GRIA2 PPI subnetwork	1.36E-04	<0.20	ZSWIM5 (4.4)	MIR3187 (4.4)
REACTOME_NICD_T	REACTOME_NICD_TRAFFICS_TO_NUC	1.51E-04	<0.20	DAG1 (3.3)	RAPGEF2 (3.3)
REACTOME_NOTCH	REACTOME_NOTCH:HLH_TRANSCRIPTION	1.51E-04	<0.20	DAG1 (3.3)	RAPGEF2 (3.3)
GO:0050767	regulation of neurogenesis	1.84E-04	<0.20	NPAS3 (4.4)	ENSG000000000000
MP:0000961	abnormal dorsal root ganglion morph	2.01E-04	<0.20	DPYSL4 (4.4)	TBX18 (2.9)
GO:0045664	regulation of neuron differentiation	2.57E-04	<0.20	NPAS3 (4.4)	LPHN3 (3.3)
ENSG00000159692	CTBP1 PPI subnetwork	2.91E-04	<0.20	ZCCHC11 (4.4)	PCDH17 (3.3)
GO:0005003	ephrin receptor activity	3.08E-04	<0.20	EFNB2 (4.4)	CDH6 (3.8)
GO:0021700	developmental maturation	3.17E-04	<0.20	SH3BP5 (3.3)	KLHL26 (2.2)
MP:0002875	decreased erythrocyte cell number	3.74E-04	<0.20	RNF123 (4.4)	UROD (4.8)
GO:0000122	negative regulation of transcription fr	3.81E-04	<0.20	IRF2BP1 (3.3)	C1orf51 (3.3)
MP:0002874	decreased hemoglobin content	3.96E-04	<0.20	UROD (5.4)	RNF123 (4.4)
GO:0048742	regulation of skeletal muscle fiber dev	3.97E-04	<0.20	ZBTB20 (3.3)	IFFO1 (2.7)
ENSG00000176444	CLK2 PPI subnetwork	4.17E-04	<0.20	RSRC2 (3.3)	SLC25A36 (3.3)
ENSG00000186153	WWOX PPI subnetwork	4.58E-04	<0.20	TARS2 (3.3)	IRF2BP1 (3.3)
ENSG00000170606	HSPA4 PPI subnetwork	4.64E-04	<0.20	PTK2 (2.9)	PRCC (2.8)
GO:0048641	regulation of skeletal muscle tissue de	4.85E-04	<0.20	IFFO1 (3.1)	ENSG000000000000
GO:0051960	regulation of nervous system develop	4.93E-04	<0.20	NPAS3 (4.4)	CDH6 (3.4)
GO:0048710	regulation of astrocyte differentiation	5.23E-04	<0.20	CDH6 (4.6)	NPAS3 (4.4)
GO:0048708	astrocyte differentiation	5.28E-04	<0.20	NPAS3 (6.6)	PP2D1 (3.6)
MP:0000774	decreased brain size	5.29E-04	<0.20	TMEM132 (4.4)	ITSN1 (4.3)
KEGG_CALCIUM_SIG	KEGG_CALCIUM_SIGNALING_PATHW	5.37E-04	<0.20	KCND3 (4.4)	CHRM4 (3.3)
ENSG00000139352	ASCL1 PPI subnetwork	5.49E-04	<0.20	TCF4 (5.5)	SOX5 (3.6)
ENSG00000010030	ETV7 PPI subnetwork	6.67E-04	<0.20	EIF2C2 (3.3)	MKRN1 (2.2)
GO:0040008	regulation of growth	7.02E-04	<0.20	ENSG000000000000	FGF18 (2.6)
GO:0051153	regulation of striated muscle cell diffe	7.23E-04	<0.20	ZBTB20 (3.3)	ENSG000000000000
ENSG00000184672	RALYL PPI subnetwork	7.28E-04	<0.20	CSMD3 (3.3)	MRPL51 (3.3)
GO:0016607	nuclear speck	7.44E-04	<0.20	RSRC2 (6.6)	PRPF38A (6.6)
GO:0042800	histone methyltransferase activity (H3	7.49E-04	<0.20	SBNO1 (4.4)	RPRD2 (3.3)
GO:0034399	nuclear periphery	7.52E-04	<0.20	MFSD10 (3.3)	ETAA1 (3.3)
GO:0016604	nuclear body	7.61E-04	<0.20	RSRC2 (5.5)	PRPF38A (5.5)
MP:0009454	impaired contextual conditioning beh	7.64E-04	<0.20	C1orf183 (3.3)	BSN (3.3)
GO:0043566	structure-specific DNA binding	8.48E-04	<0.20	ORC1 (3.1)	NCAPD2 (3.1)
MP:0008809	increased spleen iron level	9.28E-04	<0.20	UROD (5.3)	RNF123 (4.4)
GO:0001558	regulation of cell growth	9.82E-04	<0.20	CHST3 (3.3)	ENSG000000000000
GO:0003682	chromatin binding	1.03E-03	<0.20	BAHCC1 (4.4)	BBX (3.8)

B) 1e-5 GSE

ENSG00000105695	MAG PPI subnetwork	1.04E-03	<0.20	COL1A2 (7)	GPX7 (3.8)
MP:0008208	decreased pro-B cell number	1.16E-03	<0.20	C5orf13 (3)	RAB7L1 (3)
ENSG00000103994	ZFP106 PPI subnetwork	1.23E-03	>=0.20	AMBRA1 (1)	RPRD2 (3.4)
ENSG00000132535	DLG4 PPI subnetwork	1.32E-03	>=0.20	BSN (5.2)	MAPK8IP3
ENSG00000162231	NXF1 PPI subnetwork	1.76E-03	>=0.20	DHX15 (4.1)	PTBP1 (4.0)
GO:0045666	positive regulation of neuron differentiation	1.78E-03	>=0.20	KCNG1 (3.1)	ENSG00000160062
REACTOME_REGULATION_OF_INSULIN_SIGNALING	REACTOME_REGULATION_OF_INSULIN_SIGNALING	1.88E-03	>=0.20	ZSWIM5 (1)	CA10 (3.3)
MP:0008947	increased neuron number	1.91E-03	>=0.20	NTRK1 (3.1)	DPYSL4 (3.1)
ENSG00000160062	ZBTB8A PPI subnetwork	1.93E-03	>=0.20	CC2D1B (2)	MUTYH (2.1)
ENSG00000187391	MAGI2 PPI subnetwork	1.96E-03	>=0.20	CHRM4 (4.1)	CRTC1 (4.0)
GO:0008328	ionotropic glutamate receptor complex	1.97E-03	>=0.20	OPCML (5)	GRM7 (5.0)

B) 1e-5 GSE

nal P-value <=2e-3)

Reconstituted gene set Z score gene 3	Reconstituted gene set Z score gene 4	Reconstituted gene set Z score gene 5	Reconstituted gene set Z score gene 6	Reconstituted gene set Z score gene 7	Reconstituted gene set Z score gene 8	Reconstituted gene set Z score gene 9	Reconstituted gene set Z score gene 10
ODZ2 (3.9)	LPHN3 (3.)	DCC (3.6)	CADM2 (3.)	STK32C (3.)	PRKD1 (3.)	LRP1B (3.)	CHRM4 (3.1)
PRKD1 (3.)	IQSEC3 (3.)	LSAMP (3.)	HTRA1 (2.9)	BSN (2.7)	ODZ2 (2.7)	CDH6 (2.6)	FAM71E2 (2.4)
DPYSL4 (3.)	LPHN3 (3.)	CDH6 (2.9)	MIR3187 (2.)	LRP4 (2.8)	NCAM1 (2.)	LINC00354 (2.)	FGF18 (2.6)
LPHN3 (4.)	KCND3 (3.)	OPCML (3.)	LRFN5 (3.3)	NPAS3 (3.)	NEGR1 (3.)	PCDH9 (2.)	GRM7 (2.9)
LPHN3 (3.)	NCAM1 (3.)	PRKD1 (3.)	CSMD3 (3.)	ASTN2 (3.)	CA10 (2.9)	PLK2 (2.9)	CADM2 (2.8)
ENSG00000	LRP4 (2.8)	NPAS3 (2.)	PCDH17 (2.)	MRPL24 (2.)	EIF2C2 (2.)	GPR4 (2.3)	PCDH15 (2.3)
ENSG00000	LRP4 (2.8)	NPAS3 (2.)	PCDH17 (2.)	MRPL24 (2.)	EIF2C2 (2.)	GPR4 (2.3)	PCDH15 (2.3)
LPHN3 (3.)	DPYSL4 (3.)	MIR3187 (2.)	CDH6 (3.0)	NCAM1 (2.)	LMO1 (2.7)	LRP4 (2.5)	SOX5 (2.5)
NTRK1 (2.)	CDH6 (2.6)	IL11 (2.5)	FOXA1 (2.9)	PDE11A (2.)	PRKD1 (2.)	TCF4 (2.2)	WDPCP (2.1)
ENSG00000	DPYSL4 (3.)	MIR3187 (2.)	LMO1 (3.0)	LINC00354 (2.)	NCAM1 (2.)	CDH6 (2.7)	KCNG1 (2.7)
CDK19 (3.)	TCF4 (3.0)	ENSG00000	TSHZ2 (2.9)	PIK3R1 (2.)	SETBP1 (2.)	DCC (2.7)	SH3BP5 (2.6)
PLK2 (3.7)	LRFN5 (3.)	ODZ2 (3.2)	KCNG1 (3.)	LRP1B (2.9)	LRP4 (2.9)	SLITRK6 (2.)	DPYSL4 (2.5)
TRPC7 (2.8)	CBFA2T3 (2.)	TMEM190 (2.)	PROCR (2.)	GPR4 (2.3)	IQSEC3 (2.)	MECOM (2.)	NANOS2 (2.2)
APEH (3.4)	SLC2A1 (3.)	MKRN1 (3.)	ITSN1 (2.4)	SLC25A21 (2.)	SLC41A1 (2.)	SLC39A8 (2.)	RAB9BP1 (2.1)
ZNF821 (3.)	ENSG00000	TNRC18 (3.)	BAHCC1 (3.)	ZCCHC11 (2.)	BBX (2.7)	ENSG00000	SETBP1 (2.5)
SLC2A1 (4.)	MKRN1 (4.)	CHAC2 (3.)	ITSN1 (3.1)	SLC39A8 (2.)	APEH (2.4)	SH3BP5 (2.)	ASNS (2.2)
SLC44A5 (1.)	ENSG00000	COLQ (2.2)	C15orf39 (2.)	KCNH5 (2.)	JAKMIP3 (2.)	SETD8 (2.0)	C1orf183 (2.0)
TCF4 (3.1)	PIK3R1 (2.)	ENSG00000	AMBRA1 (2.)	PRCC (2.3)	ZCCHC11 (2.)	TRPC4AP (2.)	PRPF3 (2.0)
AP1G1 (3.)	IST1 (2.9)	RPRD2 (2.)	AMBRA1 (2.)	C4orf45 (2.)	TNRC18 (2.)	PTBP1 (2.6)	FIP1L1 (2.4)
PTBP1 (2.7)	EDEM2 (2.)	TOMM40 (2.)	CSMD3 (2.)	DOK6 (2.3)	PLK2 (2.1)	SLC38A2 (2.)	RNPC3 (1.9)
ZBTB20 (2.)	LRP4 (2.2)	KCNH5 (2.)	ZNF423 (2.)	ZNF438 (2.)	KCNG1 (2.)	C15orf39 (2.)	PABPC1L (1.9)
DPYSL4 (3.)	NCAM1 (3.)	MIR3187 (2.)	LPHN3 (2.9)	ENSG00000	LINC00354 (2.)	CRTC1 (2.)	SPSB4 (2.4)
SOX5 (3.6)	PP2D1 (3.)	BLID (3.5)	TMEM132 (2.)	ZSWIM5 (2.)	LRP4 (2.7)	ENSG00000	FAM71E2 (2.4)
DCC (3.3)	SOX5 (3.2)	CDH6 (3.1)	DPYSL4 (3.)	BLID (2.9)	TMEM132 (2.)	PCDH17 (2.)	ABCB9 (2.6)
NPAS3 (4.)	SOX5 (3.5)	BBX (3.2)	EFNB2 (3.2)	MACF1 (2.)	TNRC18 (2.)	LPHN3 (2.)	PHLPP2 (2.4)
GABRG1 (1.)	BSN (3.1)	CBFA2T3 (2.)	PITPNM2 (2.)	GRM7 (2.7)	KCNG1 (2.)	ODZ2 (2.5)	LRFN5 (2.5)
SETBP1 (3.)	NPAS3 (3.)	CBFA2T3 (2.)	BMP8A (2.)	DPYSL4 (2.)	CADM2 (2.)	LMO1 (2.5)	LRP4 (2.5)
PDE11A (2.)	ENSG00000	C8orf34 (2.)	CDKN3 (2.)	CADM2 (1.)	PLK3 (1.9)	ENSG00000	LSAMP (1.8)
ENSG00000	CHST3 (2.)	THBS4 (2.5)	JAKMIP3 (2.)	NPR3 (2.4)	NGF (2.3)	TBX18 (2.)	PDE11A (2.2)
MYH7B (2.)	PDE11A (2.)	PP2D1 (2.)	SETD8 (2.2)	JAKMIP3 (2.)	EXD3 (2.1)	IFFO1 (2.1)	TCF4 (2.1)
KCNG1 (2.)	PLK2 (2.5)	TOMM40 (2.)	CRTC1 (2.5)	RRNAD1 (2.)	GABRG1 (2.)	SETD8 (2.3)	PRCC (2.1)
PRPF3 (4.0)	FIP1L1 (3.)	DDX20 (3.)	ENSG00000	RPRD2 (3.)	TOE1 (3.0)	ZCCHC8 (2.)	PRCC (2.9)
ZCCHC2 (3.)	TNRC18 (3.)	ZCCHC8 (3.)	ZBTB20 (2.)	HECTD3 (2.)	CBFA2T3 (2.)	ENSG00000	C12orf65 (2.2)
RSRC2 (2.9)	FIP1L1 (2.)	PTBP1 (2.)	ZCCHC2 (2.)	RNPC3 (2.)	NCAPD2 (2.)	TOE1 (2.4)	PRPF3 (2.3)
DDX20 (3.)	FIP1L1 (3.)	C15orf39 (2.)	PRPF3 (3.3)	ZCCHC8 (3.)	TOE1 (3.1)	DHX15 (3.)	RPRD2 (3.0)
PITPNM2 (1.)	IQSEC3 (2.)	STK32C (2.)	ODZ2 (2.5)	KCND3 (2.)	MAPK8IP3 (2.)	GABRG1 (2.)	THBS4 (2.2)
NUCKS1 (2.)	MUTYH (2.)	DDB2 (2.5)	TOE1 (2.5)	SLC38A2 (2.)	KNTC1 (2.)	TBX18 (2.4)	BAHCC1 (2.3)
SLC25A21 (1.)	ITSN1 (3.2)	MKRN1 (3.)	APEH (3.0)	SLC39A8 (2.)	ZFAT (2.3)	APOC1 (2.)	CHAC2 (2.0)
ENSG00000	NGF (2.7)	ENSG00000	THBS4 (2.5)	CDH13 (2.)	PDE11A (2.)	CDH6 (2.4)	ENSG00000255117 (2.4)
RPRD2 (3.)	ZNF423 (3.)	TNRC18 (3.)	PTBP1 (3.2)	IRF2BP1 (3.)	TBX18 (2.1)	C15orf39 (2.)	SETD8 (2.6)

B) 1e-5 GSE

LAMA2 (3.)	CHST3 (3.)	BLID (3.0)	SOX5 (2.8)	BEST4 (2.6)	DAG1 (2.6)	C5orf13 (2)	TMEM132B (2.4)
TCF4 (3.1)	BAHCC1 (2)	FAM159A	PRCC (2.4)	BANK1 (2.)	PIK3R1 (2.)	PM20D1 (1)	CBFA2T3 (2.2)
ZCCHC2 (3)	ETAA1 (2.)	HARBI1 (2)	ARFGAP2	BBX (2.6)	PACSIN3 (1)	ZNF408 (2)	MACF1 (2.5)
ATP2B1 (3)	OPCML (3)	CHRM4 (3)	PITPNM2	LPHN3 (3.)	RAPGEF2	CADM2 (3)	CHN1 (3.1)
RSRC2 (3.8)	PRPF3 (3.8)	NUCKS1 (3)	TOMM34	PRPF38A (1)	IST1 (3.4)	RHOA (3.3)	HDGF (3.2)
DPYSL4 (3)	DCC (3.4)	SPSB4 (3.1)	WDR72 (2)	SOX5 (2.8)	SLC44A5 (1)	TCF4 (2.6)	SLC38A1 (2.6)
DGKZ (3.0)	WDR72 (2)	KCND3 (2.)	GRM7 (2.8)	VPS54 (2.6)	NPAS3 (2.)	LPHN3 (2.)	TCF4 (2.2)
PLK2 (3.1)	CDH6 (2.9)	NCAM1 (2)	EPB41L4A	GPR4 (2.7)	NGF (2.6)	KLHL26 (2)	FGF18 (2.6)
ZNF821 (2)	RTDR1 (2.)	ARFGAP2	HARBI1 (2)	ATG13 (2.)	UBOX5 (2.)	ARHGAP1	FIP1L1 (1.9)
BSN (3.7)	C1orf183	PITPNM2	PLK2 (3.1)	OPCML (3)	LPHN3 (3.)	ODZ2 (3.0)	MYPOP (2.8)
CA10 (4.7)	CADM2 (4)	LRP1B (4.)	CSMD3 (4.)	ASTN2 (4.)	GABRG1 (1)	CHRM4 (3)	NPAS3 (3.9)

C) 1e-5 TE

Supplementary Table 7C: Tissue enrichment analysis with DEPICT (input SNPs with p<1e-5, nominal p-value<=0.05)

MeSH term	Name	MeSH first level term	MeSH second level term	Nominal P value	False discovery rate	Tissue-specific expression Z score gene 1	Tissue-specific expression Z score gene 2	Tissue-specific expression Z score gene 3	Tissue-specific expression Z score gene 4	Tissue-specific expression Z score gene 5	Tissue-specific expression Z score gene 6	Tissue-specific expression Z score gene 7	Tissue-specific expression Z score gene 8	Tissue-specific expression Z score gene 9	Tissue-specific expression Z score gene 10
A08.186.2	Visual Cort	Nervous Sy	Central Nervous System	7.39E-04	>=0.20	ENSG0000	KCNH5 (5.1)	TMEM132	CSMD3 (4.7)	GRM7 (4.0)	LRFN5 (3.9)	RAPGEF2 (1)	OPCML (3)	ODZ2 (3.6)	LRP1B (3.3)
A08.186.2	Occipital L	Nervous Sy	Central Nervous System	8.03E-04	>=0.20	ENSG0000	KCNH5 (4.9)	TMEM132	CSMD3 (4.7)	LRFN5 (3.8)	GRM7 (3.8)	OPCML (3)	RAPGEF2 (1)	ODZ2 (3.5)	VAMP1 (3.3)
A08.186.2	Hippocam	Nervous Sy	Central Nervous System	1.62E-03	>=0.20	CSMD3 (3)	DCC (3.6)	BSN (3.6)	DOK6 (3.5)	GRM7 (3.4)	JAKMIP3 (3)	OPCML (3)	TMEM132	NCAM1 (3)	KLHL26 (3.1)
A08.186.2	Cerebral C	Nervous Sy	Central Nervous System	1.72E-03	>=0.20	CSMD3 (3)	GRM7 (3.4)	TMEM132	OPCML (3)	BSN (3.2)	LRFN5 (3.2)	CELF4 (3.1)	DCC (3.0)	DOK6 (3.0)	GABRG1 (3.0)
A08.186.2	Limbic Sys	Nervous Sy	Central Nervous System	2.04E-03	>=0.20	CSMD3 (3)	GRM7 (3.4)	DOK6 (3.3)	BSN (3.3)	OPCML (3)	DCC (3.2)	TMEM132	CELF4 (3.1)	LRFN5 (3.1)	GABRG1 (3.1)
A08.186.2	Cerebrum	Nervous Sy	Central Nervous System	2.07E-03	>=0.20	CSMD3 (3)	GRM7 (3.2)	TMEM132	OPCML (3)	BSN (3.1)	LRFN5 (3.1)	GABRG1 (3)	CELF4 (2.9)	DOK6 (2.9)	NPAS3 (2.9)
A08.186.2	Brain	Nervous Sy	Central Nervous System	2.08E-03	>=0.20	NPAS3 (2.4)	TMEM132	LRP1B (2.3)	CSMD3 (2)	ENSG0000	LPHN3 (2.2)	PCDH17 (2)	PCDH9 (2.1)	CADM2 (2)	NCAM1 (2.0)
A08.186	Central Ne	Nervous Sy	Central Nervous System	2.11E-03	>=0.20	NPAS3 (2.4)	TMEM132	LRP1B (2.3)	ENSG0000	CSMD3 (2)	LPHN3 (2.1)	PCDH17 (2)	PCDH9 (2.0)	CADM2 (2)	NCAM1 (2.0)
A08.186.2	Telenceph	Nervous Sy	Central Nervous System	2.17E-03	>=0.20	CSMD3 (3)	GRM7 (3.2)	TMEM132	OPCML (3)	BSN (3.1)	GABRG1 (3)	LRFN5 (3.0)	NPAS3 (2.9)	CELF4 (2.9)	DOK6 (2.9)
A08.186.2	Parietal Lo	Nervous Sy	Central Nervous System	2.39E-03	>=0.20	GABRG1 (3)	NPAS3 (3.1)	CELF4 (3.1)	CRTC1 (2.9)	PCDH9 (2.5)	KLHL26 (2)	LRFN5 (2.8)	OPCML (2)	CADM2 (2)	BSN (2.7)
A08.186.2	Prosencep	Nervous Sy	Central Nervous System	2.53E-03	>=0.20	CSMD3 (3)	GRM7 (3.0)	BSN (2.9)	OPCML (2)	TMEM132	JAKMIP3 (2)	GABRG1 (2)	LRFN5 (2.8)	CELF4 (2.7)	PCDH9 (2.7)
A08.186.2	Parahippo	Nervous Sy	Central Nervous System	2.76E-03	>=0.20	GRM7 (3.5)	GABRG1 (3)	CSMD3 (3)	DCC (3.3)	BSN (3.2)	KLHL26 (3)	DOK6 (3.2)	NPAS3 (3.2)	LRFN5 (3.2)	CELF4 (3.2)
A08.186.2	Entorhinal	Nervous Sy	Central Nervous System	2.76E-03	>=0.20	GRM7 (3.5)	GABRG1 (3)	CSMD3 (3)	DCC (3.3)	BSN (3.2)	KLHL26 (3)	DOK6 (3.2)	NPAS3 (3.2)	LRFN5 (3.2)	CELF4 (3.2)
A09.371.7	Retina	Sense Org	Eye	3.17E-03	>=0.20	USH2A (13)	TRPC7 (5.8)	DCC (5.6)	DPYSL4 (4)	SLC44A5 (4)	ENSG0000	ZNF821 (3)	ZSWIM5 (3)	KIAA1429	LMO1 (2.8)
A08.186.2	Temporal	Nervous Sy	Central Nervous System	3.62E-03	>=0.20	GRM7 (3.4)	GABRG1 (3)	CSMD3 (3)	BSN (3.3)	DOK6 (3.3)	DCC (3.2)	NPAS3 (3.2)	KLHL26 (3)	CELF4 (3.2)	LRFN5 (3.1)
A02.165	Cartilage	Musculosk	Cartilage	0.02	>=0.20	BLID (6.5)	NGF (6.3)	IL11 (6.2)	SOX5 (5.6)	FGF18 (5.0)	THBS4 (3.4)	SPSB4 (3.0)	SMAD3 (2)	CHST3 (2.8)	UGP2 (2.6)
A08.186.2	Brain Stem	Nervous Sy	Central Nervous System	0.03	>=0.20	CA10 (3.6)	IQSEC3 (3)	GRK4 (2.7)	ZNF821 (2)	CELF4 (2.6)	C8orf34 (2)	KCND3 (2)	CADM2 (2)	DOK6 (2.5)	ZFYVE9 (2.5)
A08.186.2	Frontal Lo	Nervous Sy	Central Nervous System	0.03	>=0.20	ENSG0000	ENSG0000	TMEM132	BSN (3.3)	CSMD3 (3)	IQSEC3 (3)	GRM7 (3.2)	DOK6 (3.2)	OPCML (3)	NICN1 (3.1)
A07.231.1	Arteries	Cardiovasq	Blood Vessels	0.03	>=0.20	TBX18 (2.5)	BTBD19 (2)	PITPNM2 (1)	CDH13 (1.9)	FNIP2 (1.8)	PROCR (1.8)	ARHGAP1 (1)	C1orf54 (1)	GPR4 (1.5)	CDH6 (1.4)
A08.186.2	Basal Gang	Nervous Sy	Central Nervous System	0.04	>=0.20	PP2D1 (4.3)	GABRG1 (3)	CADM2 (3)	PCDH15 (3)	SOX5 (3.2)	MIR3187 (1)	ZFYVE9 (3)	NCAM1 (3)	BAHCC1 (2)	LSAMP (2.7)
A08.186.2	Mesencep	Nervous Sy	Central Nervous System	0.04	>=0.20	VAMP1 (3)	NPAS3 (3.0)	NCAM1 (3)	ABCB9 (2.9)	PCDH9 (2.8)	DOK6 (2.7)	MACF1 (2)	ENSG0000	ENSG0000	CADM2 (2.5)
A08.186.2	Rhombenc	Nervous Sy	Central Nervous System	0.05	>=0.20	CA10 (4.5)	IQSEC3 (4)	C8orf34 (3)	GRK4 (3.6)	CLIP1 (3.5)	ZNF821 (3)	EPB41L4A (1)	CELF4 (3.0)	KCND3 (2.9)	OPCML (2.9)
A08.186.2	Metencep	Nervous Sy	Central Nervous System	0.05	>=0.20	CA10 (4.5)	IQSEC3 (4)	C8orf34 (3)	GRK4 (3.6)	CLIP1 (3.5)	ZNF821 (3)	EPB41L4A (1)	CELF4 (3.0)	KCND3 (2.9)	OPCML (2.9)
A07.541.5	Heart Valv	Cardiovasq	Heart	0.05	>=0.20	BLID (4.2)	LAMA2 (3)	C1orf54 (2)	SETBP1 (2)	CDH13 (2.3)	MECOM (2)	TSHZ2 (2.1)	ZBTB20 (2)	C8orf34 (2)	ETAA1 (2.0)
A07.541.5	Aortic Valv	Cardiovasq	Heart	0.05	>=0.20	BLID (4.2)	LAMA2 (3)	C1orf54 (2)	SETBP1 (2)	CDH13 (2.3)	MECOM (2)	TSHZ2 (2.1)	ZBTB20 (2)	C8orf34 (2)	ETAA1 (2.0)
A08.186.2	Cerebellur	Nervous Sy	Central Nervous System	0.05	>=0.20	CA10 (4.7)	IQSEC3 (4)	CLIP1 (4.1)	GRK4 (3.9)	C8orf34 (3)	ZNF821 (3)	EPB41L4A (1)	KCND3 (3)	C5orf13 (3)	OPCML (3.0)

Supplementary Table 7D: Gene prioritisation with DEPICT (input SNPs for BP_MA with p<5e-8)

Locus	Nr of genes in locus	Chromosome and position	GWAS P value	Ensembl gene ID	Gene symbol	Nominal P value	Gene closest to lead SNP	Top cis eQTL SNP (Westra et al. Nature Genetics 2014)	False discovery rate
rs1921117	1	chr5:3119	9.86E-09	ENSG000000000000	CDH6	6.10E-03	TRUE	rs7722943	>0.20
rs1047597	1	chr5:1708	5.34E-09	ENSG000000000000	FGF18	7.04E-03	TRUE	rs919325	>0.20
rs9804988	1	chr12:236	1.31E-16	ENSG000000000000	SOX5	0.01	TRUE	-	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG000000000000	-	0.04	FALSE	-	>0.20
rs7613469	1	chr13:863	2.93E-08	ENSG000000000000	SLITRK6	0.06	TRUE	-	>0.20
rs2219837	1	chr10:737	2.51E-12	ENSG000000000000	CHST3	0.09	TRUE	-	>0.20
rs2672596	1	chr10:124	4.06E-11	ENSG000000000000	HTRA1	0.13	TRUE	rs2292627	>0.20
rs1204765	1	chr20:496	1.91E-08	ENSG000000000000	KCNG1	0.15	TRUE	rs4809820	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	DAG1	0.19	FALSE	rs6784820	>0.20
rs7226995	1	chr18:498	9.86E-09	ENSG000000000000	DCC	0.22	FALSE	-	>0.20
rs4974563	2	chr4:1145	2.44E-08	ENSG000000000000	SPON2	0.22	FALSE	rs7684536	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG000000000000	FOXA1	0.23	FALSE	-	>0.20
rs1087026	3	chr10:133	9.78E-09	ENSG000000000000	DPYSL4	0.23	TRUE	rs2101613	>0.20
rs1940720	2	chr11:112	3.16E-08	ENSG000000000000	-	0.29	TRUE	-	>0.20
rs1087026	3	chr10:133	9.78E-09	ENSG000000000000	STK32C	0.3	FALSE	rs7099831	>0.20
rs1150768	1	chr9:1402	9.75E-09	ENSG000000000000	EXD3	0.32	TRUE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	BSN	0.38	FALSE	-	>0.20
rs1940720	2	chr11:112	3.16E-08	ENSG000000000000	NCAM1	0.39	FALSE	rs1711531	>0.20
rs4974563	2	chr4:1145	2.44E-08	ENSG000000000000	-	0.4	TRUE	-	>0.20
rs7266676	1	chr8:6924	5.77E-14	ENSG000000000000	C8orf34	0.41	FALSE	-	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG000000000000	SLC25A21	0.41	FALSE	rs848087	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG000000000000	TTC6	0.55	FALSE	-	>0.20
rs1313509	2	chr4:1023	3.49E-08	ENSG000000000000	BANK1	0.64	FALSE	rs1703197	>0.20
rs1313509	2	chr4:1023	3.49E-08	ENSG000000000000	SLC39A8	0.68	TRUE	rs7655493	>0.20
rs1095648	1	chr8:1303	5.88E-15	ENSG000000000000	-	0.7	TRUE	-	>0.20
rs1087026	3	chr10:133	9.78E-09	ENSG000000000000	JAKMIP3	0.77	FALSE	rs1114624	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	NICN1	0.8	FALSE	rs3870339	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	APEH	0.86	FALSE	rs3197999	>0.20
rs1268085	2	chr8:9549	8.78E-09	ENSG000000000000	-	0.86	FALSE	-	>0.20
rs324300	1	chr11:296	4.80E-09	ENSG000000000000	-	0.88	TRUE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	AMT	0.89	FALSE	rs1568661	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	TCTA	0.92	FALSE	rs9881860	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	RNF123	0.94	FALSE	-	>0.20
rs8022156	5	chr14:371	4.80E-10	ENSG000000000000	MIPOL1	0.94	TRUE	rs1884803	>0.20
rs4703253	1	chr5:1028	2.01E-08	ENSG000000000000	NUDT12	0.96	TRUE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	BSN-AS2	0.98	FALSE	-	>0.20
rs6779524	9	chr3:4939	2.36E-08	ENSG000000000000	RHOA	0.98	TRUE	-	>0.20
rs1268085	2	chr8:9549	8.78E-09	ENSG000000000000	KIAA1429	1	TRUE	-	>0.20

Supplementary Table 7E: Gene set enrichment analysis with DEPICT (input SNPs with p<5e-8, nominal P-value <=1e-3)

Original gene set ID	Original gene set description	Nominal P value	False discovery rate	Reconstituted gene set gene 1	Reconstituted gene set gene 2	Reconstituted gene set gene 3	Reconstituted gene set gene 4	Reconstituted gene set gene 5	Reconstituted gene set gene 6	Reconstituted gene set gene 7	Reconstituted gene set gene 8	Reconstituted gene set gene 9	Reconstructed gene set Z score gene 10
ENSG0000	ENDOG PPI subnetwork	8.38E-05	>=0.20	FGF18 (1.5)	JAKMIP3 (1)	TCTA (1.3)	SPON2 (1.1)	SLC25A21	STK32C (1)	DCC (1.0)	ENSG0000	ENSG0000	BSN-AS2 (0.8)
MP:00094	paraparesis	1.16E-04	>=0.20	NCAM1 (2)	SLC25A21	MIPOL1 (1)	ENSG0000	BSN (1.4)	JAKMIP3 (1)	DPYSL4 (1)	HTRA1 (1.1)	SOX5 (1.1)	ENSG00000229140 (1.1)
MP:00011	abnormal uterus morphology	2.18E-04	>=0.20	CHST3 (3.1)	SLC39A8 (1)	KCNG1 (2.1)	HTRA1 (2.1)	ENSG0000	SOX5 (1.7)	JAKMIP3 (1)	SLTRK6 (1)	ENSG0000	ENSG00000247416 (1.3)
ENSG0000	PAPD4 PPI subnetwork	2.31E-04	>=0.20	ENSG0000	STK32C (1)	FGF18 (1.5)	CDH6 (1.4)	SLC25A21	EXD3 (1.3)	ENSG0000	FOXA1 (1.1)	RNF123 (1)	BSN-AS2 (1.2)
ENSG0000	ASCL1 PPI subnetwork	2.50E-04	>=0.20	SOX5 (3.6)	DPYSL4 (2)	BANK1 (2.1)	ENSG0000	ENSG0000	ENSG0000	KCNG1 (1.1)	CHST3 (1.4)	HTRA1 (1.1)	EXD3 (1.2)
GO:00488	regulation of axon extension involved in axon guidance	2.79E-04	>=0.20	ENSG0000	HTRA1 (2.1)	MIPOL1 (1)	CDH6 (1.9)	KCNG1 (1.1)	ENSG0000	DCC (1.5)	C8orf34 (1)	SOX5 (1.1)	FGF18 (1.0)
GO:00220	central nervous system myelination	2.81E-04	>=0.20	SOX5 (2.8)	ENSG0000	CHST3 (2.1)	ENSG0000	NCAM1 (1)	CDH6 (1.6)	ENSG0000	NICN1 (1.4)	BSN (0.8)	SLC39A8 (0.8)
GO:00322	axon ensheathment in central nervous system	2.81E-04	>=0.20	SOX5 (2.8)	ENSG0000	CHST3 (2.1)	ENSG0000	NCAM1 (1)	CDH6 (1.6)	ENSG0000	NICN1 (1.4)	BSN (0.8)	SLC39A8 (0.8)
GO:00080	cell recognition	4.28E-04	>=0.20	ENSG0000	KCNG1 (2.1)	CDH6 (2.1)	DPYSL4 (1)	BANK1 (1.1)	NCAM1 (1)	DCC (1.5)	SOX5 (1.4)	NICN1 (1.3)	STK32C (1.2)
GO:00100	glial cell differentiation	4.52E-04	>=0.20	SOX5 (4.0)	CDH6 (3.6)	ENSG0000	DPYSL4 (3)	CHST3 (2.1)	DCC (2.2)	NCAM1 (2)	STK32C (2)	ENSG0000	SLC25A21 (1.8)
GO:00074	axonal fasciculation	4.84E-04	>=0.20	KCNG1 (3.3)	SOX5 (3.3)	SLTRK6 (3)	CDH6 (2.9)	ENSG0000	DPYSL4 (2)	BSN (2.2)	ENSG0000	DCC (1.9)	MIPOL1 (1.8)
GO:00217	glial cell development	4.87E-04	>=0.20	SOX5 (3.1)	CHST3 (2.1)	ENSG0000	STK32C (2)	ENSG0000	NCAM1 (2)	DPYSL4 (2)	MIPOL1 (1)	CDH6 (1.6)	C8orf34 (1.3)
MP:00014	hypoactivity	4.98E-04	>=0.20	STK32C (1)	BSN (1.7)	CDH6 (1.6)	NCAM1 (1)	SLTRK6 (1)	JAKMIP3 (1)	FGF18 (1.3)	RNF123 (1)	DPYSL4 (1)	C8orf34 (1.1)
GO:00420	gliogenesis	5.01E-04	>=0.20	SOX5 (4.0)	DPYSL4 (3)	CDH6 (3.2)	ENSG0000	ENSG0000	CHST3 (2.4)	NCAM1 (2)	DCC (1.9)	STK32C (1)	SLC25A21 (1.6)
GO:00487	astrocyte differentiation	5.33E-04	>=0.20	DCC (3.3)	SOX5 (3.2)	CDH6 (3.1)	DPYSL4 (3)	ENSG0000	ENSG0000	STK32C (1)	MIPOL1 (1)	KCNG1 (1.1)	ENSG00000258708 (1.5)
GO:00080	neuron recognition	5.76E-04	>=0.20	DCC (3.8)	SLTRK6 (3)	KCNG1 (2.1)	DPYSL4 (2)	ENSG0000	CDH6 (2.7)	SOX5 (2.7)	NCAM1 (2)	ENSG0000	NICN1 (2.1)
GO:00150	glucuronosyltransferase activity	6.05E-04	>=0.20	SOX5 (2.3)	NUDT12 (1)	ENSG0000	TCTA (1.7)	HTRA1 (1.1)	SPON2 (1.1)	NCAM1 (1)	KCNG1 (1.1)	SLC39A8 (1)	FOXA1 (1.3)
REACTOME	REACTOME_REGULATION_OF_INSULIN:LIKE_GROWTH	8.86E-04	>=0.20	SPON2 (4.1)	FGF18 (2.9)	C8orf34 (2)	CDH6 (2.0)	FOXA1 (2.1)	ENSG0000	TTC6 (1.7)	HTRA1 (1.1)	SLTRK6 (1)	ENSG00000212997 (1.3)
GO:00510	negative regulation of secretion	9.56E-04	>=0.20	JAKMIP3 (1)	BSN-AS2 (1)	SLC39A8 (1)	SOX5 (1.7)	ENSG0000	ENSG0000	SLTRK6 (1)	STK32C (1)	KCNG1 (1.1)	FGF18 (1.1)
ENSG0000	SAA4 PPI subnetwork	9.81E-04	>=0.20	FOXA1 (4.1)	SPON2 (2.1)	CHST3 (2.1)	DCC (2.0)	SLTRK6 (1)	HTRA1 (1.1)	TTC6 (1.5)	CDH6 (1.5)	DAG1 (1.3)	AMT (1.3)

Supplementary Table 7F: Tissue enrichment analysis with DEPICT (input SNPs with p<5e-8, nominal p-value<=0.07)

MeSH term	Name	MeSH first level term	MeSH second level term	Nominal P value	False discovery rate	Tissue-specific expression Z score gene 1	Tissue-specific expression Z score gene 2	Tissue-specific expression Z score gene 3	Tissue-specific expression Z score gene 4	Tissue-specific expression Z score gene 5	Tissue-specific expression Z score gene 6	Tissue-specific expression Z score gene 7	Tissue-specific expression Z score gene 8	Tissue-specific expression Z score gene 9	Tissue-specific expression Z score gene 10
A05.360.3	Endometri	Urogenita	Genitalia	3.00E-02	>=0.20	SPON2 (2.1)	FGF18 (1.3)	SLTRK6 (1.0)	SOX5 (1.0)	AMT (0.8)	SLC39A8 (0.7)	CHST3 (0.7)	DAG1 (0.6)	C8orf34 (0.5)	HTRA1 (0.5)
A05.360.4	Germ Cell	Urogenita	Genitalia	5.00E-02	>=0.20	CHST3 (2.1)	SLC39A8 (1.3)	SPON2 (1.0)	SLTRK6 (0.9)	FGF18 (0.9)	SOX5 (0.8)	NUDT12 (0.7)	HTRA1 (0.7)	MIPOL1 (0.5)	C8orf34 (0.5)
A02.165	Cartilage	Musculos	Cartilage	5.00E-02	>=0.20	SOX5 (5.6)	FGF18 (5.4)	CHST3 (2.8)	SLC39A8 (1.0)	ENSG000000000000	ENSG000000000000	MIPOL1 (0.7)	KCNG1 (0.7)	HTRA1 (0.7)	ENSG000000258708 (0.3)
A10.165.1	Subcutane	Tissues	Connective Tissue	6.00E-02	>=0.20	C8orf34 (2.1)	TCTA (1.7)	SOX5 (1.3)	SPON2 (1.1)	EXD3 (1.3)	ENSG000000000000	BANK1 (1.0)	HTRA1 (1.0)	RHOA (1.1)	AMT (1.0)
A10.165.1	Abdomina	Tissues	Connective Tissue	6.00E-02	>=0.20	C8orf34 (2.1)	TCTA (1.7)	SOX5 (1.3)	SPON2 (1.1)	EXD3 (1.3)	ENSG000000000000	BANK1 (1.0)	HTRA1 (1.1)	RHOA (1.1)	AMT (1.0)
A11.872.6	Neural Ste	Cells	Stem Cells	6.00E-02	>=0.20	ENSG000000000000	DPYSL4 (4.4)	CDH6 (2.9)	DCC (2.8)	KIAA1429 (1.0)	CHST3 (2.0)	DAG1 (2.0)	RHOA (1.3)	NICN1 (1.1)	RNF123 (1.0)
A03.556.5	Salivary G	Digestive	Gastrointestinal Tract	7.00E-02	>=0.20	SLC39A8 (1.0)	KCNG1 (2.1)	STK32C (2.1)	SLTRK6 (1.0)	EXD3 (1.9)	ENSG000000000000	AMT (1.4)	DAG1 (1.0)	APEH (0.9)	SOX5 (0.7)
A05.360.3	Uterus	Urogenita	Genitalia	7.00E-02	>=0.20	SPON2 (1.1)	FGF18 (1.3)	AMT (0.7)	SLTRK6 (0.9)	SOX5 (0.6)	DAG1 (0.6)	HTRA1 (0.7)	RHOA (0.4)	CHST3 (0.4)	C8orf34 (0.3)
A10.165.1	Subcutane	Tissues	Connective Tissue	7.00E-02	>=0.20	C8orf34 (2.1)	ENSG000000000000	SOX5 (1.3)	TCTA (1.3)	SPON2 (1.1)	RHOA (1.2)	HTRA1 (1.1)	AMT (1.0)	BANK1 (1.0)	EXD3 (0.9)
A10.165.1	Adipose Ti	Tissues	Connective Tissue	7.00E-02	>=0.20	C8orf34 (2.1)	ENSG000000000000	SOX5 (1.3)	TCTA (1.3)	SPON2 (1.1)	RHOA (1.2)	HTRA1 (1.1)	AMT (1.0)	BANK1 (1.0)	EXD3 (0.9)
A14.549.8	Tongue	Stomatog	Mouth	7.00E-02	>=0.20	ENSG000000000000	DCC (1.5)	KCNG1 (1.1)	EXD3 (1.4)	SPON2 (1.1)	ENSG000000000000	SLTRK6 (1.0)	ENSG000000000000	STK32C (0.9)	HTRA1 (0.4)
A05.360	Genitalia	Urogenita	Genitalia	7.00E-02	>=0.20	FGF18 (1.3)	SPON2 (1.1)	ENSG000000000000	FOXA1 (0.9)	MIPOL1 (0.7)	DAG1 (0.8)	TTC6 (0.8)	KIAA1429 (0.7)	C8orf34 (0.7)	SLTRK6 (0.7)
A15.145.2	Erythrocyt	Hemic and	Blood	7.00E-02	>=0.20	SLC25A21 (1.0)	ENSG000000000000	ENSG000000000000	STK32C (1.0)	ENSG000000000000	EXD3 (1.6)	SLC39A8 (1.0)	KCNG1 (1.0)		
A07.541.3	Heart Atri	Cardiovas	Heart	0.07	>=0.20	ENSG000000000000	AMT (2.2)	NCAM1 (2.0)	ENSG000000000000	NICN1 (1.9)	CHST3 (1.4)	SLC39A8 (1.0)	KIAA1429 (1.0)	ENSG000000000000	KCNG1 (1.1)

Supplementary Tables 8. MAGMA v1.6 results.

GenomicRisk loci - loci defined by FUMA tool.

1. Gene analysis

SNPs are mapped to 19436 protein coding genes (with unique ensembl ID) if SNPs are located within gene body.

All parameters were set as default (SNP-wise (mean) model for gene test).

2. Gene-set analysis

Gene sets were obtained from MsigDB v5.2. Total of 10894 gene sets (Curated gene sets (4728) and GO terms (6166)) were tested.

Curated gene sets consists of 9 data resources including KEGG, Reactome and BioCarta (http://software.broadinstitute.org/gsea/msigdb/collection_details.jsp#C2 for details).

GO terms consists of three categories, biological processes (bp), cellular components (cc) and molecular functions (mf).

All parameters were set as default (competitive test).

3. Tissue expression analysis

Gene expression was obtained from GTEx v6.

Average gene-expression per tissue type were used as gene covariate to test positive relationship between gene expression in a specific tissue type and genetic associations.

MAGMA gene-property test was performed for average expression (log2 transformed RPKM with pseudocount 1 after winsorization at 50) of 30 general tissue types and 53 specific tissue types conditioning on average expression across all tissue types.

Supplementary Table 8A. Genomic risk loci defined by independent lead SNPs and maximum distance between their LD block

GenomicL	uniqID	rsID	chr	pos	p	start	end	nSNPs	nGWASSNPs	nIndSigSNPs	IndSigSNPs	nLeadSNPs	LeadSNPs
1	3:49450449:C:T	rs6779524	3	49450449	2.36E-08	49385417	49731861	112	103	1	rs6779524	1	rs6779524
2	4:1138153:C:T	rs4974563	4	1138153	2.44E-08	1107478	1179213	21	16	1	rs4974563	1	rs4974563
3	4:103198082:A:G	rs13135092	4	1.03E+08	3.49E-08	1.03E+08	1.03E+08	6	2	1	rs13135092	1	rs13135092
4	4:140243320:A:G	rs189350593	4	1.4E+08	3.81E-08	1.4E+08	1.4E+08	2	2	1	rs189350593	1	rs189350593
5	5:30876763:A:G	rs1921117	5	30876763	9.86E-09	30848710	30880177	7	6	1	rs1921117	1	rs1921117
6	5:102892224:C:T	rs4703253	5	1.03E+08	2.01E-08	1.03E+08	1.03E+08	15	13	1	rs4703253	1	rs4703253
7	5:170859228:C:G	rs10475978	5	1.71E+08	5.34E-09	1.71E+08	1.71E+08	8	6	1	rs10475978	1	rs10475978
8	6:34592090:A:G	rs6907508	6	34592090	3.07E-10	34548206	34831761	90	83	1	rs6907508	1	rs6907508
9	8:69574165:C:T	rs1865442	8	69574165	3.91E-14	69558467	69657438	70	65	3	rs1865442;rs7000878;rs1369229	2	rs1865442;rs1369229
10	8:95589340:A:G	rs4735297	8	95589340	8.57E-09	95496030	95631555	77	67	1	rs4735297	1	rs4735297
11	8:130717716:A:G	rs10956487	8	1.31E+08	5.88E-15	1.31E+08	1.31E+08	101	89	4	rs10956487;rs12056383;rs12679359;rs117	2	rs10956487;rs117981565
12	9:140262424:C:T	rs11507683	9	1.4E+08	9.75E-09	1.4E+08	1.4E+08	16	14	1	rs11507683	1	rs11507683
13	10:73762673:C:T	rs2219837	10	73762673	2.51E-12	73732665	73840357	132	109	2	rs2219837;rs3180	1	rs2219837
14	10:124226793:A:G	rs2672596	10	1.24E+08	4.06E-11	1.24E+08	1.24E+08	10	9	2	rs2672596;rs2248799	1	rs2672596
15	10:133968063:C:T	rs10870267	10	1.34E+08	9.78E-09	1.34E+08	1.34E+08	53	34	1	rs10870267	1	rs10870267
16	11:29674831:A:G	rs324300	11	29674831	4.80E-09	29633243	29675343	5	5	1	rs324300	1	rs324300
17	11:112860893:A:T	rs7121047	11	1.13E+08	3.16E-08	1.13E+08	1.13E+08	102	95	1	rs7121047	1	rs7121047
18	12:23982559:C:T	rs9804988	12	23982559	1.31E-16	23936398	23982559	13	12	2	rs9804988;rs12308843	1	rs9804988
19	13:87294817:G:T	rs76134699	13	87294817	2.93E-08	87204405	87910447	6	4	1	rs76134699	1	rs76134699
20	14:37657148:C:T	rs8022156	14	37657148	4.80E-10	37448052	38075174	438	388	3	rs8022156;rs2180599;rs7161228	1	rs8022156
21	18:50895755:A:G	rs7226995	18	50895755	9.86E-09	50555931	50995585	470	401	2	rs7226995;rs11663824	1	rs7226995
22	20:49719603:G:T	rs1204765	20	49719603	1.91E-08	49716117	49719603	2	1	1	rs1204765	1	rs1204765

Genomic locus : Index of genomic rick loci.

uniqID : Unique ID of SNPs consists of chr:position:allele1:allele2 where alleles are alphabetically ordered.

rsID : rsID of the top lead SNP based on dbSNP build 146.

chr : chromosome of top lead SNP

pos : position of top lead SNP on hg19

p : P-value of top lead SNP (from the input file).

start : Start position of the locus

end : End postion of the locus

nSNPs : The number of unique canidate SNPs in the genomic locus, including non-GWAS-tagged SNPs (which are extracted from 1000G).

nGWASSNPs : The number of the GWAS-tagged candidate SNPs within the genomic locus. This is a subset of "nSNPs".

nIndSigSNPs : The number of the independent significant SNPs in the genomic locus ($r^2 <$ user defined parameter)

IndSigSNPs : rsID of independent significant SNPs in the genomic locus

nLeadSNPs : The number of lead SNPs in the genomic locus ($r^2 < 0.1$)

LeadSNPs : rsID of lead SNPs in the genomic locus

Supplementary Table 8B. Genes defined by MAGMA

GENE	CHR	START	STOP	NSNPS	NPARAM	N	ZSTAT	P	SYMBOL	Bonferroni FDR
ENSG00000187323	18	49856542	51067784	6513	176	453862	7.988	6.86E-16	DCC	1.25E-11 1.25E-11
ENSG00000165084	8	69232957	69741257	1889	165	453862	7.3162	1.28E-13	C8orf34	2.33E-09 7.46E-10
ENSG00000122863	10	73714123	73783322	314	38	453862	7.2972	1.47E-13	CHST3	2.68E-09 7.46E-10
ENSG00000151338	14	37657118	38031566	1123	49	453862	7.2825	1.64E-13	MIPOL1	2.98E-09 7.46E-10
ENSG00000107742	10	73808793	73858790	193	38	453862	6.8848	2.89E-12	SPOCK2	5.26E-08 1.05E-08
ENSG00000164061	3	49581922	49718978	314	39	453862	6.3376	1.17E-10	BSN	2.13E-06 3.55E-07
ENSG00000147697	8	1.31E+08	1.31E+08	314	48	453862	6.2757	1.74E-10	GSDMC	3.17E-06 4.00E-07
ENSG00000188385	10	1.34E+08	1.34E+08	659	87	453862	6.2744	1.76E-10	JAKMIP3	3.20E-06 4.00E-07
ENSG00000233276	3	49384609	49406033	57	21	453862	6.2041	2.75E-10	GPX1	5.01E-06 5.56E-07
ENSG00000112874	5	1.03E+08	1.03E+08	84	21	453862	6.1711	3.39E-10	NUDT12	6.17E-06 6.17E-07
ENSG00000156427	5	1.71E+08	1.71E+08	199	56	453862	6.1452	3.99E-10	FGF18	7.26E-06 6.60E-07
ENSG00000052795	4	1.6E+08	1.6E+08	442	48	453862	6.093	5.54E-10	FNIP2	1.01E-05 8.40E-07
ENSG00000067560	3	49386578	49460431	208	34	453862	5.9991	9.92E-10	RHOA	1.81E-05 1.39E-06
ENSG00000145029	3	49450379	49476759	76	20	453862	5.9599	1.26E-09	NICN1	2.29E-05 1.64E-06
ENSG00000145022	3	49439639	49463908	61	16	453862	5.9374	1.45E-09	TCTA	2.64E-05 1.76E-06
ENSG00000196569	6	1.29E+08	1.3E+08	2470	144	453862	5.8768	2.09E-09	LAMA2	3.80E-05 2.38E-06
ENSG00000146555	7	3331080	4318632	6399	203	453862	5.8161	3.01E-09	SDK1	5.48E-05 3.09E-06
ENSG00000145020	3	49444211	49470186	61	16	453862	5.8077	3.17E-09	AMT	5.77E-05 3.09E-06
ENSG00000196821	6	34545065	34674636	562	45	453862	5.8042	3.23E-09	C6orf106	5.88E-05 3.09E-06
ENSG00000183032	14	37137636	37652071	2121	156	453862	5.7744	3.86E-09	SLC25A21	7.03E-05 3.51E-06
ENSG00000149294	11	1.13E+08	1.13E+08	1514	105	453862	5.7587	4.24E-09	NCAM1	7.72E-05 3.67E-06
ENSG00000129514	14	38049189	38079245	89	28	453862	5.7085	5.70E-09	FOXA1	0.000104 4.72E-06
ENSG00000173402	3	49496146	49583048	213	35	453862	5.6687	7.19E-09	DAG1	0.000131 5.69E-06
ENSG00000051825	12	1.24E+08	1.24E+08	450	30	453862	5.6406	8.47E-09	MPHOSPH9	0.000154 6.42E-06
ENSG00000145864	5	1.61E+08	1.61E+08	1084	84	453862	5.612	1.00E-08	GABRB2	0.000182 7.28E-06
ENSG00000027644	1	1.57E+08	1.57E+08	119	41	453862	5.5935	1.11E-08	INSRR	0.000202 7.41E-06
ENSG00000164068	3	49716932	49768962	135	38	453862	5.5934	1.11E-08	RNF123	0.000202 7.41E-06
ENSG00000123908	8	1.42E+08	1.42E+08	563	82	453862	5.588	1.15E-08	AGO2	0.000209 7.41E-06
ENSG00000102984	16	71883583	71939239	181	39	453862	5.5839	1.18E-08	ZNF821	0.000215 7.41E-06
ENSG00000224470	16	71869894	71929171	194	40	453862	5.5528	1.41E-08	ATXN1L	0.000257 8.55E-06
ENSG00000204315	6	32086484	32108068	71	32	453862	5.475	2.19E-08	FKBPL	0.000399 1.27E-05
ENSG00000173531	3	49711380	49736934	49	18	453862	5.4709	2.24E-08	MST1	0.000408 1.27E-05
ENSG00000130287	19	19312782	19373042	215	43	453862	5.4246	2.90E-08	NCAN	0.000528 1.57E-05
ENSG00000170604	19	46376866	46399376	99	26	453862	5.4209	2.96E-08	IRF2BP1	0.000539 1.57E-05
ENSG00000124562	6	34715183	34751571	211	26	453862	5.4176	3.02E-08	SNRPC	0.00055 1.57E-05
ENSG00000078814	20	33553206	33600240	178	32	453862	5.4087	3.17E-08	MYH7B	0.000577 1.60E-05
ENSG00000069018	5	1.36E+08	1.36E+08	739	62	453862	5.3952	3.42E-08	TRPC7	0.000622 1.68E-05
ENSG00000175224	11	46628826	46706368	172	44	453862	5.373	3.87E-08	ATG13	0.000704 1.85E-05
ENSG00000175216	11	46754598	46877847	291	40	453862	5.3578	4.21E-08	CKAP5	0.000766 1.96E-05
ENSG00000175220	11	46688630	46732165	126	38	453862	5.3506	4.38E-08	ARHGAP1	0.000797 1.99E-05
ENSG00000241404	6	32122360	32146058	81	28	453862	5.3433	4.56E-08	EGFL8	0.00083 1.99E-05
ENSG00000254636	10	1.24E+08	1.24E+08	92	22	453862	5.3418	4.60E-08	ARMS2	0.000837 1.99E-05
ENSG00000110497	11	46407964	46625675	452	71	453862	5.3341	4.80E-08	AMBRA1	0.000874 1.99E-05
ENSG00000090621	1	40016488	40052462	150	37	453862	5.334	4.80E-08	PABPC4	0.000874 1.99E-05
ENSG00000159674	4	1150720	1212750	241	61	453862	5.3285	4.95E-08	SPON2	0.000901 2.00E-05
ENSG00000066827	8	1.35E+08	1.36E+08	1178	88	453862	5.3076	5.55E-08	ZFAT	0.00101 2.18E-05
ENSG00000115365	2	2.11E+08	2.11E+08	273	29	453862	5.3054	5.62E-08	LANCL1	0.001023 2.18E-05
ENSG00000221988	6	32111218	32144011	114	40	453862	5.2807	6.43E-08	PPT2	0.001117 2.40E-05
ENSG00000130921	12	1.24E+08	1.24E+08	188	23	453862	5.2798	6.47E-08	C12orf65	0.001178 2.40E-05
ENSG00000085788	8	38072736	38143076	146	35	453862	5.255	7.40E-08	DDHD2	0.001347 2.66E-05
ENSG00000182149	16	71869899	71927913	379	40	453862	5.2517	7.54E-08	IST1	0.001372 2.66E-05
ENSG00000143369	1	1.5E+08	1.5E+08	87	25	453862	5.2501	7.60E-08	ECM1	0.001383 2.66E-05
ENSG00000198400	1	1.57E+08	1.57E+08	274	77	453862	5.2447	7.83E-08	NTRK1	0.001425 2.69E-05
ENSG00000165046	8	38233725	38277045	113	28	453862	5.2364	8.19E-08	LETM2	0.001491 2.76E-05
ENSG00000183763	3	49856034	49904007	105	28	453862	5.2156	9.16E-08	TRAIP	0.001667 3.03E-05
ENSG00000140832	16	71650064	71686017	128	33	453862	5.1871	1.07E-07	MARVELD3	0.001948 3.48E-05
ENSG00000176095	3	49751727	49833975	214	38	453862	5.1762	1.13E-07	IP6K1	0.002057 3.61E-05
ENSG00000196782	4	1.41E+08	1.41E+08	1646	221	453862	5.1727	1.15E-07	MAML3	0.002093 3.61E-05
ENSG00000213676	6	32055953	32106030	163	53	453862	5.1634	1.21E-07	ATF6B	0.002202 3.73E-05
ENSG00000027869	1	1.57E+08	1.57E+08	98	31	453862	5.152	1.29E-07	SH2D2A	0.002348 3.91E-05
ENSG00000172663	11	67221824	67246743	97	20	453862	5.1226	1.51E-07	TMEM134	0.002748 4.42E-05
ENSG00000258388	6	32111622	32149755	136	38	453862	5.1207	1.52E-07	PPT2-EGFL8	0.002767 4.42E-05
ENSG00000164123	4	1.6E+08	1.6E+08	686	51	453862	5.1194	1.53E-07	C4orf45	0.002785 4.42E-05
ENSG00000158406	6	26271283	26295762	150	30	453862	5.1022	1.68E-07	HIST1H4H	0.003058 4.73E-05
ENSG00000156735	8	38024051	38080819	141	24	453862	5.1006	1.69E-07	BAG4	0.003076 4.73E-05
ENSG00000175544	11	67209877	67236699	104	21	453862	5.0957	1.74E-07	CABP4	0.003167 4.80E-05
ENSG00000176020	3	49744267	49771349	80	24	453862	5.0864	1.82E-07	AMIGO3	0.003313 4.87E-05
ENSG00000173540	3	49744277	49771384	80	24	453862	5.0864	1.82E-07	GMPPB	0.003313 4.87E-05
ENSG00000150471	4	62056976	62954053	3250	205	453862	5.0812	1.88E-07	LPHN3	0.003422 4.96E-05
ENSG00000109756	4	1.6E+08	1.6E+08	858	75	453862	5.0753	1.93E-07	RAPGEF2	0.003513 5.02E-05

ENSG000000258708	14	37631093	37653016	73	16	453862	5.0566	2.13E-07	SLC25A21-AS1	0.003877	5.46E-05
ENSG000000134569	11	46868419	46950193	205	37	453862	5.046	2.26E-07	LRP4	0.004113	5.71E-05
ENSG000000175514	11	67208772	67230200	87	19	453862	5.0229	2.55E-07	GPR152	0.004641	6.36E-05
ENSG00000011304	19	787075	822327	187	47	453862	5.0128	2.68E-07	PTBP1	0.004878	6.50E-05
ENSG000000204310	6	32125989	32155873	109	31	453862	5.011	2.71E-07	AGPAT1	0.004932	6.50E-05
ENSG000000100991	20	33580207	33690674	390	32	453862	5.0103	2.72E-07	TRPC4AP	0.004951	6.50E-05
ENSG000000164076	3	49885421	49917655	77	25	453862	5.0078	2.75E-07	CAMKV	0.005005	6.50E-05
ENSG000000175324	8	38010839	38044248	88	26	453862	4.989	3.04E-07	LSM1	0.005533	7.09E-05
ENSG000000147535	8	38110648	38136761	58	21	453862	4.933	4.05E-07	PPAPDC1B	0.007371	9.19E-05
ENSG000000163576	3	19910964	19998517	411	46	453862	4.9329	4.05E-07	EFHB	0.007371	9.19E-05
ENSG000000110711	11	67240512	67268574	89	21	453862	4.931	4.09E-07	AIP	0.007444	9.19E-05
ENSG000000169398	8	1.42E+08	1.42E+08	1107	58	453862	4.9212	4.30E-07	PTK2	0.007826	9.54E-05
ENSG000000185019	20	3078219	3150842	265	41	453862	4.9188	4.35E-07	UBOX5	0.007917	9.54E-05
ENSG000000175213	11	46712368	46737462	67	22	453862	4.9138	4.47E-07	ZNF408	0.008136	9.59E-05
ENSG000000196277	3	6801688	7793215	4533	340	453862	4.9133	4.48E-07	GRMT	0.008154	9.59E-05
ENSG000000182095	7	5336421	5475045	682	147	453862	4.8941	4.94E-07	TNRC18	0.008991	0.000105
ENSG000000134198	1	1.16E+08	1.16E+08	243	47	453862	4.8857	5.15E-07	TSPAN2	0.009374	0.000108
ENSG000000130208	19	45407504	45432606	72	29	453862	4.8761	5.41E-07	APOC1	0.009847	0.000111
ENSG000000143294	1	1.57E+08	1.57E+08	248	43	453862	4.874	5.47E-07	PRCC	0.009956	0.000111
ENSG000000164062	3	49701435	49731396	64	19	453862	4.8732	5.49E-07	APEH	0.009992	0.000111
ENSG000000187492	3	49818165	49847268	78	27	453862	4.8528	6.09E-07	CDHR4	0.011084	0.000122
ENSG000000144535	2	2.33E+08	2.33E+08	1721	57	453862	4.8401	6.49E-07	DIS3L2	0.011812	0.000128
ENSG000000165379	14	42066773	42383752	1423	71	453862	4.8267	6.94E-07	LRFN5	0.012631	0.000136
ENSG000000180210	11	46730730	46771056	121	27	453862	4.8247	7.01E-07	F2	0.012759	0.000136
ENSG000000148516	10	31597424	31828742	537	41	453862	4.8197	7.19E-07	ZEB1	0.013087	0.000138
ENSG000000166949	15	67346101	67497533	570	110	453862	4.8068	7.67E-07	SMAD3	0.01396	0.000145
ENSG000000167522	16	89324038	89566969	867	80	453862	4.8007	7.91E-07	ANKRD11	0.014397	0.000148
ENSG000000110697	11	67249239	67283734	100	29	453862	4.7844	8.57E-07	PITPNM1	0.015598	0.000159
ENSG000000142700	1	50873222	50899172	71	18	453862	4.771	9.16E-07	DMRTA2	0.016672	0.000168
ENSG000000127415	4	970785	1008316	168	49	453862	4.7609	9.63E-07	IDUA	0.017528	0.000174
ENSG000000139364	12	1.26E+08	1.26E+08	1953	217	453862	4.7601	9.67E-07	TMEM132B	0.0176	0.000174
ENSG000000169764	2	64058074	64128696	246	60	453862	4.7567	9.84E-07	UGP2	0.01791	0.000176
ENSG000000172725	11	67195519	67221292	84	22	453862	4.7433	1.05E-06	CORO1B	0.019111	0.000186
ENSG000000077782	8	38258656	38336352	248	69	453862	4.7424	1.06E-06	FGFR1	0.019293	0.000186
ENSG000000070961	12	89971828	90113077	353	49	453862	4.7328	1.11E-06	ATP2B1	0.020203	0.000192
ENSG000000147548	8	38117215	38249790	307	35	453862	4.7236	1.16E-06	WHSC1L1	0.021113	0.000199
ENSG000000214655	10	75535340	75571551	68	25	453862	4.7178	1.19E-06	ZSWIM8	0.021659	0.000202
ENSG000000149091	11	46344455	46412104	178	58	453862	4.7128	1.22E-06	DGKZ	0.022205	0.000206
ENSG000000204314	6	32106136	32132150	99	39	453862	4.7017	1.29E-06	PRRT1	0.023479	0.000215
ENSG000000129993	16	88931266	89053612	786	77	453862	4.6906	1.36E-06	CBFA2T3	0.024753	0.000225
ENSG000000170608	19	46357247	46387055	114	35	453862	4.6795	1.44E-06	FOXA3	0.026209	0.000234
ENSG000000166747	16	71752913	71853104	375	48	453862	4.6795	1.44E-06	AP1G1	0.026209	0.000234
ENSG000000146918	7	1.58E+08	1.59E+08	419	38	453862	4.6614	1.57E-06	NCAPG2	0.028576	0.000253
ENSG000000163950	4	1684527	1724282	181	33	453862	4.6503	1.66E-06	SLBP	0.030214	0.000265
ENSG000000114316	3	49305264	49388145	177	39	453862	4.6428	1.72E-06	USP4	0.031306	0.000271
ENSG000000172366	16	681813	708474	100	31	453862	4.6419	1.73E-06	FAM195A	0.031488	0.000271
ENSG000000107679	10	1.24E+08	1.24E+08	321	36	453862	4.6343	1.79E-06	PLEKHA1	0.03258	0.000278
ENSG000000134259	1	1.16E+08	1.16E+08	318	65	453862	4.6181	1.94E-06	NGF	0.03531	0.000299
ENSG000000134294	12	46741972	46776650	99	29	453862	4.6095	2.02E-06	SLC38A2	0.036766	0.000309
ENSG000000127580	16	724622	750444	81	22	453862	4.6035	2.08E-06	WDR24	0.037858	0.000315
ENSG000000140015	14	63163287	63578755	1701	138	453862	4.594	2.17E-06	KCNH5	0.039496	0.000326
ENSG000000196628	18	52879562	53342018	1324	119	453862	4.5891	2.23E-06	TCF4	0.040588	0.00033
ENSG000000167791	11	67276383	67300899	77	26	453862	4.5885	2.23E-06	CABP2	0.040588	0.00033
ENSG000000149600	20	31280493	31341803	222	29	453862	4.5856	2.26E-06	COMMID7	0.041134	0.000332
ENSG00000002822	7	1845429	2282878	2846	72	453862	4.5808	2.32E-06	MAD1L1	0.042226	0.000335
ENSG000000176182	19	46383278	46415862	173	38	453862	4.5804	2.32E-06	MYPOP	0.042226	0.000335
ENSG000000164638	7	5304000	5356501	292	61	453862	4.5658	2.49E-06	SLC29A4	0.04532	0.000357
ENSG000000187145	1	1.5E+08	1.5E+08	148	21	453862	4.5639	2.51E-06	MRPS21	0.045685	0.000357
ENSG000000143374	1	1.5E+08	1.5E+08	156	24	453862	4.5563	2.60E-06	TARS2	0.047323	0.000367
ENSG00000065060	6	34749857	34860915	527	38	453862	4.528	2.98E-06	UHRF1BP1	0.054239	0.000417
ENSG000000248483	5	93060508	93087343	63	23	453862	4.5022	3.36E-06	POU5F2	0.061155	0.000466
ENSG000000102935	16	49511435	49901830	1496	207	453862	4.5012	3.38E-06	ZNF423	0.061519	0.000466
ENSG000000125266	13	1.07E+08	1.07E+08	197	63	453862	4.496	3.46E-06	EFNB2	0.062975	0.000473
ENSG000000120708	5	1.35E+08	1.35E+08	197	32	453862	4.4915	3.54E-06	TGFBI	0.064432	0.000481
ENSG000000134744	1	52863954	53029159	436	41	453862	4.4858	3.63E-06	ZCCHC11	0.06607	0.000487
ENSG000000143321	1	1.57E+08	1.57E+08	142	38	453862	4.4854	3.64E-06	HDGF	0.066252	0.000487
ENSG000000113391	5	92943775	93457404	1229	58	453862	4.482	3.70E-06	FAM172A	0.067344	0.000492
ENSG000000127585	16	732500	765829	112	28	453862	4.4743	3.83E-06	FBXL16	0.06971	0.000505
ENSG000000125388	4	2955335	3052474	494	48	453862	4.4668	3.97E-06	GRK4	0.072258	0.00052
ENSG000000165985	10	16545742	16574004	131	27	453862	4.4546	4.20E-06	C1QL3	0.076444	0.000546
ENSG000000257017	16	72078491	72104954	97	24	453862	4.4409	4.48E-06	HP	0.08154	0.000578
ENSG000000172586	10	75531805	75553410	42	17	453862	4.4307	4.70E-06	CHCHD1	0.085545	0.000602
ENSG000000144445	2	2.11E+08	2.11E+08	350	88	453862	4.4079	5.22E-06	KANSL1L	0.095009	0.000664

ENSG00000113296	5 79277134 79389110	426	41	453862	4.3865	5.76E-06	THBS4	0.104838	0.000728
ENSG00000159140	21 34904924 34959812	136	54	453862	4.382	5.88E-06	SON	0.107022	0.000738
ENSG00000090975	12 1.23E+08 1.24E+08	561	39	453862	4.3725	6.14E-06	PITPNM2	0.111754	0.000765
ENSG00000187609	9 1.4E+08 1.4E+08	616	138	453862	4.3708	6.19E-06	EXD3	0.112664	0.000766
ENSG00000161999	16 721671 744529	77	26	453862	4.3682	6.26E-06	JMJD8	0.113938	0.00077
ENSG00000166896	12 58325324 58361052	134	19	453862	4.3556	6.64E-06	XRCC6BP1	0.120855	0.000809
ENSG00000104413	8 95643302 95729694	390	42	453862	4.3544	6.67E-06	ESRP1	0.121401	0.000809
ENSG00000164078	3 49914435 49951299	75	21	453862	4.3305	7.44E-06	MST1R	0.135415	0.000897
ENSG00000080709	5 1.14E+08 1.14E+08	595	90	453862	4.3257	7.60E-06	KCNN2	0.138328	0.00091
ENSG00000114439	3 1.07E+08 1.08E+08	998	74	453862	4.3211	7.76E-06	BBX	0.14124	0.000923
ENSG00000135365	11 45940871 46152985	600	54	453862	4.3044	8.37E-06	PHF21A	0.152342	0.000989
ENSG00000162877	1 2.06E+08 2.06E+08	153	44	453862	4.3024	8.45E-06	PM20D1	0.153798	0.000992
ENSG00000042781	1 2.16E+08 2.17E+08	3305	252	453862	4.2951	8.73E-06	USH2A	0.158895	0.001019
ENSG00000093010	22 19919130 19967498	302	60	453862	4.2885	8.99E-06	COMT	0.163627	0.001038
ENSG00000204580	6 30834198 30877933	273	35	453862	4.2881	9.01E-06	DDR1	0.163991	0.001038
ENSG00000164077	3 49936302 49977606	85	21	453862	4.2855	9.12E-06	MON1A	0.165993	0.001044
ENSG00000105662	19 18784487 18903004	454	73	453862	4.2834	9.20E-06	CRTC1	0.167449	0.001047
ENSG00000166507	10 75551669 75581589	62	18	453862	4.2755	9.54E-06	NDST2	0.173638	0.001078
ENSG00000145217	4 962861 997228	145	46	453862	4.2727	9.66E-06	SLC26A1	0.175822	0.001084
ENSG00000151640	10 1.34E+08 1.34E+08	244	47	453862	4.2716	9.71E-06	DPYSL4	0.176732	0.001084
ENSG00000111328	12 1.24E+08 1.24E+08	134	24	453862	4.2666	9.92E-06	CDK2AP1	0.180554	0.001101
ENSG00000103266	16 720224 742870	81	26	453862	4.2545	1.05E-05	STUB1	0.191111	0.001151
ENSG00000183049	10 12381481 12887545	2744	257	453862	4.2541	1.05E-05	CAMK1D	0.191111	0.001151
ENSG00000139323	12 89803495 89929801	427	39	453862	4.2492	1.07E-05	POC1B	0.194751	0.001166
ENSG00000150977	12 1.24E+08 1.24E+08	118	39	453862	4.2422	1.11E-05	RILPL2	0.202031	0.001203
ENSG00000213780	6 30865961 30891883	162	22	453862	4.2344	1.15E-05	GTF2H4	0.209312	0.001239
ENSG00000040199	16 71661738 71768604	386	42	453862	4.2322	1.16E-05	PHLPP2	0.211132	0.001242
ENSG00000088808	14 1.04E+08 1.04E+08	505	31	453862	4.2288	1.18E-05	PPP1R13B	0.214772	0.001249
ENSG00000168477	6 31998931 32093111	318	58	453862	4.2272	1.18E-05	TNXB	0.214772	0.001249
ENSG00000159147	21 34921848 34971014	112	46	453862	4.2264	1.19E-05	DONSON	0.216592	0.001252
ENSG00000140830	16 72068188 72138330	290	37	453862	4.2233	1.20E-05	TXNL4B	0.218412	0.001255
ENSG00000160472	19 55878204 55899612	99	31	453862	4.2079	1.29E-05	TMEM190	0.234793	0.001342
ENSG00000198822	7 86263230 86504200	798	79	453862	4.2054	1.30E-05	GRM3	0.236613	0.001344
ENSG00000166033	10 1.24E+08 1.24E+08	370	52	453862	4.2027	1.32E-05	HTRA1	0.240253	0.001357
ENSG00000110492	11 46392306 46415375	50	22	453862	4.2003	1.33E-05	MDK	0.242073	0.00136
ENSG00000153820	2 2.29E+08 2.29E+08	1012	61	453862	4.1989	1.34E-05	SPHKAP	0.243893	0.001363
ENSG00000261701	16 72078522 72121145	170	40	453862	4.1982	1.35E-05	HPR	0.245714	0.001365
ENSG00000048828	9 96204004 96338397	555	48	453862	4.1937	1.37E-05	FAM120A	0.249354	0.001378
ENSG00000171604	5 1.39E+08 1.39E+08	161	42	453862	4.1931	1.38E-05	CXXC5	0.251174	0.00138
ENSG00000163125	1 1.5E+08 1.5E+08	587	31	453862	4.1873	1.41E-05	RPRD2	0.256634	0.001402
ENSG00000169371	15 75880424 75928810	144	27	453862	4.1764	1.48E-05	SNUPN	0.269375	0.00146
ENSG0000001617	3 50182478 50236508	133	27	453862	4.1732	1.50E-05	SEMA3F	0.273015	0.00146
ENSG00000111371	12 46566846 46673800	324	72	453862	4.1729	1.50E-05	SLC38A1	0.273015	0.00146
ENSG00000181163	5 1.71E+08 1.71E+08	159	18	453862	4.1728	1.50E-05	NPM1	0.273015	0.00146
ENSG00000163909	1 40079825 40115617	132	52	453862	4.1724	1.51E-05	HEYL	0.274835	0.001462
ENSG00000029559	4 88710733 88743074	128	41	453862	4.144	1.71E-05	IBSP	0.311237	0.001647
ENSG00000152932	5 57868048 58165213	1222	115	453862	4.1374	1.76E-05	RAB3C	0.320338	0.001686
ENSG00000141664	18 60180240 60264942	325	50	453862	4.1284	1.83E-05	ZCCHC2	0.333078	0.001744
ENSG00000188211	11 17363273 17408888	188	33	453862	4.1267	1.84E-05	NCR3LG1	0.334898	0.001744
ENSG00000124507	6 34423916 34513006	425	72	453862	4.126	1.85E-05	PAC SIN1	0.336719	0.001745
ENSG00000152217	18 42250138 42658475	1240	192	453862	4.1147	1.94E-05	SETBP1	0.353099	0.001811
ENSG00000198931	16 88865747 88888352	179	33	453862	4.1142	1.94E-05	APRT	0.353099	0.001811
ENSG00000177363	11 62443874 62467371	64	17	453862	4.1061	2.01E-05	LRRN4CL	0.36584	0.001857
ENSG00000100206	22 38904954 38976291	199	53	453862	4.1059	2.01E-05	DMC1	0.36584	0.001857
ENSG00000196968	10 75522049 75550009	58	16	453862	4.1046	2.03E-05	FUT11	0.36948	0.001865
ENSG00000231852	6 31996042 32019447	49	30	453862	4.1018	2.05E-05	CYP21A2	0.373121	0.001865
ENSG00000103269	16 715666 738268	95	26	453862	4.1014	2.05E-05	RHBDL1	0.373121	0.001865
ENSG00000176986	10 75494120 75541919	112	27	453862	4.1007	2.06E-05	SEC24C	0.374941	0.001865
ENSG00000215251	20 3117165 3150543	117	37	453862	4.0983	2.08E-05	FASTKD5	0.378581	0.001874
ENSG00000182179	3 49832640 49861379	69	28	453862	4.0956	2.11E-05	UBA7	0.384041	0.001882
ENSG00000204308	6 32136131 32161930	86	24	453862	4.094	2.12E-05	RNF5	0.385861	0.001882
ENSG00000166268	12 70209084 70362877	746	65	453862	4.0935	2.12E-05	MYRFL	0.385861	0.001882
ENSG00000167513	16 88859621 88885666	173	40	453862	4.0907	2.15E-05	CDT1	0.391322	0.001919
ENSG00000257594	12 89903185 89930039	109	20	453862	4.0862	2.19E-05	GALNT4	0.398602	0.001916
ENSG00000259075	12 89903185 89930039	109	20	453862	4.0862	2.19E-05	POC1B-GALNT4	0.398602	0.001916
ENSG00000109184	4 52699166 52793003	256	38	453862	4.0833	2.22E-05	DCUN1D4	0.404062	0.001933
ENSG00000160161	19 19639057 19667468	106	26	453862	4.0757	2.29E-05	CILP2	0.416803	0.001983
ENSG00000214338	6 1.28E+08 1.28E+08	363	48	453862	4.074	2.31E-05	SOGA3	0.420443	0.001983
ENSG00000135426	12 55331802 55388530	294	28	453862	4.0739	2.31E-05	TESPA1	0.420443	0.001983
ENSG00000127418	4 993724 1030685	184	50	453862	4.0703	2.35E-05	FGFR1	0.427724	0.002006
ENSG00000148660	10 75562259 75644343	192	44	453862	4.0684	2.37E-05	CAMK2G	0.431364	0.002006
ENSG00000187079	11 12685969 12976298	957	71	453862	4.0683	2.37E-05	TEAD1	0.431364	0.002006
ENSG00000117360	1 1.5E+08 1.5E+08	202	28	453862	4.0597	2.46E-05	PRPF3	0.447745	0.002073

ENSG00000133302	5 93944052	94085141	530	36	453862	4.0575	2.48E-05	ANKRD32	0.451385	0.00208
ENSG00000180423	11 46614411	46649459	72	28	453862	4.054	2.52E-05	HARBI1	0.458665	0.002104
ENSG00000169490	8 38836327	38864343	96	19	453862	4.0483	2.58E-05	TM2D2	0.469586	0.002134
ENSG00000167487	19 18737775	18791309	236	49	453862	4.048	2.58E-05	KLHL26	0.469586	0.002134
ENSG00000182704	11 76483295	76519198	115	26	453862	4.0444	2.62E-05	TSKU	0.476866	0.002158
ENSG00000087269	4 2929660	2975112	234	46	453862	4.0414	2.66E-05	NOP14	0.484147	0.002171
ENSG00000102967	16 72032487	72068954	163	35	453862	4.0411	2.66E-05	DHODH	0.484147	0.002171
ENSG00000129951	19 802518	831967	125	37	453862	4.0319	2.77E-05	LPPR3	0.504168	0.002251
ENSG00000165730	10 70577298	70665188	371	52	453862	4.0259	2.84E-05	STOX1	0.516908	0.002297
ENSG00000055163	5 1.57E+08	1.57E+08	583	43	453862	4.0173	2.94E-05	CYFIP2	0.535109	0.002368
ENSG00000137411	6 30866019	30904236	254	22	453862	4.0159	2.96E-05	VARS2	0.53875	0.002373
ENSG00000213402	11 67192981	67215538	65	18	453862	4.0093	3.05E-05	PTPRCAP	0.555131	0.002435
ENSG00000161996	16 689311	727833	168	24	453862	4.0036	3.12E-05	WDR90	0.567871	0.00248
ENSG00000134532	12 23672440	24113966	1696	218	453862	3.9968	3.21E-05	SOX5	0.584252	0.002545
ENSG00000204305	6 32138745	32162101	77	21	453862	3.995	3.23E-05	AGER	0.587892	0.002545
ENSG00000070081	11 17219700	17381521	475	59	453862	3.9884	3.33E-05	NUCB2	0.606093	0.002601
ENSG00000179915	2 50135643	51269674	4999	217	453862	3.9879	3.33E-05	NRXN1	0.606093	0.002601
ENSG00000165912	11 47189076	47217994	78	23	453862	3.9863	3.36E-05	PAC SIN3	0.611554	0.002613
ENSG00000172260	1 71851623	72758417	2928	171	453862	3.9805	3.44E-05	NEGR1	0.626114	0.002664
ENSG00000184949	22 38964125	39062634	328	31	453862	3.9786	3.47E-05	FAM227A	0.631575	0.002676
ENSG00000144959	3 1.72E+08	1.72E+08	397	90	453862	3.9726	3.55E-05	NCEH1	0.646136	0.002723
ENSG00000222047	10 75659727	75692535	104	24	453862	3.9725	3.56E-05	C10orf55	0.647956	0.002723
ENSG00000143450	1 1.52E+08	1.52E+08	96	16	453862	3.971	3.58E-05	OAZ3	0.651596	0.002723
ENSG00000168000	11 62447747	62487317	119	29	453862	3.9704	3.59E-05	BSCL2	0.653416	0.002723
ENSG00000183955	12 1.24E+08	1.24E+08	172	35	453862	3.951	3.89E-05	SETD8	0.708019	0.002938
ENSG00000132356	5 40749481	40808476	171	38	453862	3.9484	3.93E-05	PRKAA1	0.715299	0.002956
ENSG00000088899	20 3133263	3164192	117	39	453862	3.947	3.96E-05	LZTS3	0.72076	0.002966
ENSG00000114349	3 50219045	50243949	50	13	453862	3.9418	4.04E-05	GNAT1	0.73532	0.003014
ENSG00000168936	4 1707679	1733085	160	23	453862	3.9391	4.09E-05	TMEM129	0.744421	0.003038
ENSG00000091656	8 77583454	77789521	677	75	453862	3.9325	4.20E-05	ZFH X4	0.764442	0.003107
ENSG00000100711	14 1.04E+08	1.04E+08	125	49	453862	3.9308	4.23E-05	ZFYVE21	0.769902	0.003112
ENSG00000126215	14 1.04E+08	1.04E+08	138	45	453862	3.9302	4.24E-05	X RCC3	0.771722	0.003112
ENSG00000164692	7 94013873	94070544	231	67	453862	3.9284	4.28E-05	COL1A2	0.779003	0.003129
ENSG00000104472	8 1.42E+08	1.42E+08	89	34	453862	3.9244	4.35E-05	CHRAC1	0.791744	0.003167
ENSG00000196352	1 2.07E+08	2.08E+08	188	33	453862	3.9231	4.37E-05	CD55	0.795384	0.003169
ENSG00000069275	1 2.06E+08	2.06E+08	216	48	453862	3.9219	4.39E-05	NUCKS1	0.799024	0.003171
ENSG00000250067	19 19617036	19658390	152	24	453862	3.9099	4.62E-05	YJEFN3	0.840886	0.003324
ENSG00000139910	14 26902299	27076960	529	35	453862	3.9023	4.76E-05	NOVA1	0.866368	0.003411
ENSG00000204304	6 32142512	32167963	90	27	453862	3.8994	4.82E-05	PBX2	0.877288	0.00344
ENSG00000255330	6 1.28E+08	1.28E+08	362	43	453862	3.8841	5.14E-05	SOGA3	0.935531	0.00364
ENSG00000143303	1 1.57E+08	1.57E+08	82	30	453862	3.8837	5.14E-05	RRNAD1	0.935531	0.00364
ENSG00000234857	11 62447747	62504856	172	33	453862	3.8801	5.22E-05	HNRNPUL2-BSCL2	0.950092	0.003683
ENSG00000125378	14 54406454	54435479	116	41	453862	3.8789	5.25E-05	BMP4	0.955553	0.003689
ENSG00000186010	19 19616545	19654285	139	22	453862	3.8691	5.46E-05	NDUFA13	0.993775	0.003822
ENSG00000127603	1 39536988	39962849	1408	69	453862	3.8685	5.48E-05	MACF1	0.997415	0.003822
ENSG00000169495	8 38821683	38856181	101	17	453862	3.867	5.51E-05	HTRA4	1	0.003828
ENSG00000100226	22 39091728	39144304	170	32	453862	3.8626	5.61E-05	GTPBP1	1	0.003882
ENSG00000168242	6 26263144	26283622	97	27	453862	3.8592	5.69E-05	HIST1H2B1	1	0.003923
ENSG00000167302	17 79192077	79222891	129	32	453862	3.8538	5.82E-05	ENTHD2	1	0.003997
ENSG00000224877	17 79203039	79225081	82	28	453862	3.845	6.03E-05	C17orf89	1	0.004126
ENSG00000185614	3 49830687	49852463	53	23	453862	3.8348	6.28E-05	FAM212A	1	0.004281
ENSG00000188993	4 52849868	52893786	121	32	453862	3.8327	6.34E-05	LRRC66	1	0.004297
ENSG00000221978	1 1311091	1344708	131	24	453862	3.8324	6.35E-05	CCNL2	1	0.004297
ENSG00000149182	11 47175848	47208676	102	29	453862	3.8293	6.43E-05	ARFGAP2	1	0.004335
ENSG00000165752	10 1.34E+08	1.34E+08	854	120	453862	3.8242	6.56E-05	STK32C	1	0.004406
ENSG00000133065	1 2.06E+08	2.06E+08	184	44	453862	3.8169	6.76E-05	SLC41A1	1	0.004523
ENSG00000157500	3 57251765	57317496	209	46	453862	3.81	6.95E-05	APPL1	1	0.004634
ENSG00000114013	3 1.22E+08	1.22E+08	249	67	453862	3.8082	7.00E-05	CD86	1	0.00464
ENSG00000142188	21 34794792	34862318	313	30	453862	3.8079	7.01E-05	TMEM50B	1	0.00464
ENSG00000143314	1 1.57E+08	1.57E+08	70	24	453862	3.8032	7.14E-05	MRPL24	1	0.004709
ENSG00000132485	1 71518974	71556980	121	32	453862	3.8	7.23E-05	ZRANB2	1	0.004747
ENSG00000146216	6 43201418	43265997	265	52	453862	3.7996	7.25E-05	TTBK1	1	0.004747
ENSG00000134852	4 56284070	56423305	657	28	453862	3.7982	7.29E-05	CLOCK	1	0.004756
ENSG00000173163	2 62105859	62384382	859	50	453862	3.7896	7.54E-05	COMMD1	1	0.004901
ENSG00000186960	14 29231910	29292493	113	59	453862	3.7838	7.72E-05	C14orf23	1	0.005
ENSG00000159128	21 34765202	34861655	416	45	453862	3.7794	7.86E-05	IFNGR2	1	0.005068
ENSG00000172915	13 35506424	36257159	2796	102	453862	3.7788	7.88E-05	NBEA	1	0.005068
ENSG00000139865	14 38055052	38520647	1699	146	453862	3.767	8.26E-05	TTC6	1	0.005275
ENSG00000100221	22 39071548	39107561	124	19	453862	3.767	8.26E-05	JOSD1	1	0.005275
ENSG00000159208	1 1.5E+08	1.5E+08	74	16	453862	3.7632	8.39E-05	C10orf51	1	0.005339
ENSG00000185046	12 99110235	1E+08	4619	294	453862	3.7624	8.42E-05	ANKS1B	1	0.00534
ENSG00000141570	17 77755931	77785482	90	43	453862	3.7606	8.47E-05	CBX8	1	0.005353
ENSG00000164604	7 1.13E+08	1.13E+08	101	25	453862	3.7573	8.59E-05	GPR85	1	0.005404

ENSG00000084207	11	67341066	67364131	118	20	453862	3.7567	8.61E-05	GSTP1	1	0.005404
ENSG00000163069	4	52876872	52914648	99	37	453862	3.7556	8.65E-05	SGCB	1	0.00541
ENSG00000204335	2	1.72E+08	1.72E+08	87	22	453862	3.7525	8.75E-05	SP5	1	0.005454
ENSG00000134748	1	52860236	52896511	68	22	453862	3.7492	8.87E-05	PRPF38A	1	0.00551
ENSG0000025772	20	43560771	43599127	143	45	453862	3.7477	8.92E-05	TOMM34	1	0.005522
ENSG00000256018	6	26261146	26281612	96	25	453862	3.7439	9.06E-05	HIST1H3G	1	0.005557
ENSG00000186448	3	44616380	44699963	220	44	453862	3.7428	9.10E-05	ZNF197	1	0.005557
ENSG00000100216	22	39067953	39090818	88	13	453862	3.7426	9.11E-05	TOMM22	1	0.005557
ENSG00000184445	12	1.23E+08	1.23E+08	385	44	453862	3.7422	9.12E-05	KNTC1	1	0.005557
ENSG00000175305	8	95881998	95918906	156	33	453862	3.7418	9.13E-05	CCNE2	1	0.005557
ENSG00000118007	3	1.36E+08	1.36E+08	1232	70	453862	3.741	9.16E-05	STAG1	1	0.005557
ENSG00000170144	2	1.78E+08	1.78E+08	71	25	453862	3.7378	9.28E-05	HNRNPA3	1	0.005611
ENSG00000168830	6	87637024	87736349	367	41	453862	3.7364	9.33E-05	HTR1E	1	0.005623
ENSG00000122861	10	75658935	75687255	86	22	453862	3.7331	9.46E-05	PLAU	1	0.005683
ENSG00000197183	20	31020862	31182876	497	68	453862	3.7287	9.62E-05	C20orf112	1	0.00576
ENSG00000177692	21	34850497	34874027	82	24	453862	3.7274	9.67E-05	DNAJC28	1	0.005771
ENSG00000112812	6	27205480	27234403	122	30	453862	3.7257	9.74E-05	PRSS16	1	0.005793
ENSG00000235608	4	1386720	1410119	75	23	453862	3.7163	0.000101	NKX1-1	1	0.005993
ENSG00000184162	19	19302225	19324233	62	23	453862	3.7151	0.000102	NR2C2AP	1	0.006002
ENSG00000146955	7	1.4E+08	1.4E+08	151	41	453862	3.7118	0.000103	RAB19	1	0.006026
ENSG00000169955	16	30527244	30556668	55	29	453862	3.7114	0.000103	ZNF747	1	0.006026
ENSG0000021826	2	2.11E+08	2.12E+08	856	72	453862	3.7113	0.000103	CPS1	1	0.006026
ENSG00000140983	16	708086	734174	119	19	453862	3.7108	0.000103	RHOT2	1	0.006026
ENSG00000150873	2	11263179	11296916	203	34	453862	3.7097	0.000104	C2orf50	1	0.006033
ENSG0000013810	4	1713227	1756898	286	24	453862	3.7081	0.000104	TACC3	1	0.006052
ENSG00000100242	22	39120730	39200148	254	53	453862	3.7027	0.000107	SUN2	1	0.006162
ENSG00000198039	7	64320550	64401344	407	25	453862	3.6977	0.000109	ZNF273	1	0.00624
ENSG00000101251	20	13819893	13987089	678	69	453862	3.6974	0.000109	SEL1L2	1	0.00624
ENSG00000162976	2	11285324	11329000	197	51	453862	3.6971	0.000109	PQLC3	1	0.00624
ENSG00000233493	19	55880613	55905966	132	36	453862	3.6937	0.000111	TMEM238	1	0.006306
ENSG00000164761	8	1.2E+08	1.2E+08	216	38	453862	3.6799	0.000117	TNFRSF11B	1	0.006635
ENSG00000175029	10	1.27E+08	1.27E+08	968	126	453862	3.6771	0.000118	CTBP2	1	0.006688
ENSG00000169375	15	75651720	75758183	239	54	453862	3.6755	0.000119	SIN3A	1	0.00671
ENSG00000185104	1	50895150	51435935	1341	71	453862	3.6663	0.000123	FAF1	1	0.006934
ENSG00000167797	11	67263968	67286120	66	25	453862	3.6624	0.000125	CDK2AP2	1	0.007019
ENSG00000081177	14	696468228	69719075	204	37	453862	3.6604	0.000126	EXD2	1	0.007039
ENSG00000130204	19	45383826	45416946	144	38	453862	3.6601	0.000126	TOMM40	1	0.007039
ENSG00000179588	16	88509725	88613424	501	90	453862	3.6493	0.000131	ZFPMP1	1	0.007297
ENSG00000136457	17	48531857	48556327	92	26	453862	3.6493	0.000132	CHAD	1	0.007297
ENSG00000178796	1	1.52E+08	1.52E+08	131	33	453862	3.6477	0.000132	RIIAD1	1	0.007319
ENSG00000143436	1	1.52E+08	1.52E+08	73	14	453862	3.6449	0.000134	MRPL9	1	0.007377
ENSG0000010292	12	6592522	6651121	283	33	453862	3.6439	0.000134	NCAPD2	1	0.007384
ENSG00000131634	16	1568689	1615581	260	35	453862	3.6394	0.000137	TMEM204	1	0.007469
ENSG00000144792	3	44609715	44651186	131	27	453862	3.6393	0.000137	ZNF660	1	0.007469
ENSG00000118557	16	72136056	72220777	346	41	453862	3.638	0.000137	PMFBP1	1	0.007469
ENSG00000101104	20	43528703	43597676	268	51	453862	3.6378	0.000137	PABC1L	1	0.007469
ENSG00000115361	2	2.11E+08	2.11E+08	98	36	453862	3.6371	0.000138	ACADL	1	0.007469
ENSG00000078403	10	21813094	22042559	500	101	453862	3.6343	0.000139	MLLT10	1	0.007528
ENSG00000128191	22	20057755	20109400	245	37	453862	3.6325	0.00014	DGCR8	1	0.007557
ENSG00000167377	16	71471500	71506998	120	30	453862	3.6306	0.000141	ZNF23	1	0.00759
ENSG00000130203	19	45399011	45422650	89	30	453862	3.6252	0.000144	APOE	1	0.007728
ENSG00000198765	1	1.15E+08	1.16E+08	547	45	453862	3.6244	0.000145	SYCP1	1	0.007731
ENSG00000175634	11	67185931	67212872	78	27	453862	3.6221	0.000146	RPSKB2	1	0.007776
ENSG00000148219	9	1.19E+08	1.2E+08	4568	272	453862	3.6206	0.000147	ASTN2	1	0.007797
ENSG00000214753	11	62470102	62504821	103	29	453862	3.6192	0.000148	HNRNPUL2	1	0.007816
ENSG00000261459	16	30527244	30556173	54	29	453862	3.618	0.000148	ZNF747	1	0.007821
ENSG00000178093	19	19613227	19636838	83	18	453862	3.6176	0.000149	TSSK6	1	0.007821
ENSG00000064490	19	19293008	19322678	92	30	453862	3.6129	0.000151	RFXANK	1	0.007942
ENSG00000100591	14	77914213	77945817	151	28	453862	3.6086	0.000154	AHSA1	1	0.00805
ENSG00000182196	12	1.23E+08	1.23E+08	62	13	453862	3.5995	0.000159	ARL6IP4	1	0.008314
ENSG00000136874	9	1.03E+08	1.03E+08	228	37	453862	3.5983	0.00016	STX17	1	0.008329
ENSG00000171522	5	40669600	40703837	114	22	453862	3.5969	0.000161	PTGER4	1	0.00833
ENSG00000100211	22	39042641	39079859	173	12	453862	3.5968	0.000161	CBY1	1	0.00833
ENSG00000130720	9	1.34E+08	1.34E+08	307	55	453862	3.5946	0.000162	FIBCD1	1	0.008356
ENSG00000066135	1	44105829	44181186	221	43	453862	3.5945	0.000163	KDM4A	1	0.008356
ENSG00000113638	5	40704577	40766077	177	33	453862	3.592	0.000164	TTC33	1	0.008413
ENSG00000168631	6	30898749	30931998	172	45	453862	3.5912	0.000165	DPCR1	1	0.008415
ENSG00000151353	2	657335	687439	113	34	453862	3.5867	0.000167	TMEM18	1	0.008537
ENSG00000164944	8	95489921	95575757	418	30	453862	3.5858	0.000168	KIAA1429	1	0.008544
ENSG00000176715	16	89144783	89232254	650	44	453862	3.5829	0.000167	ACSF3	1	0.008614
ENSG00000161896	6	33679444	33724762	337	40	453862	3.5788	0.000173	IP6K3	1	0.008724
ENSG00000107771	10	86078342	86288273	834	40	453862	3.5769	0.000174	CCSER2	1	0.008765
ENSG00000118508	6	1.47E+08	1.47E+08	78	25	453862	3.5759	0.000175	RAB32	1	0.008769

ENSG00000080603	16	30699530	30765602	114	48	453862	3.5753	0.000175	SRCAP	1	0.008769
ENSG00000239388	3	57292375	57336710	130	30	453862	3.5741	0.000176	ASB14	1	0.008785
ENSG00000129535	14	24539316	24594223	155	55	453862	3.5575	0.000187	NRL	1	0.009334
ENSG00000181752	11	55916870	55937793	57	12	453862	3.554	0.00019	OR8K5	1	0.009387
ENSG00000111271	12	1.12E+08	1.12E+08	163	34	453862	3.5535	0.00019	ACAD10	1	0.009387
ENSG00000227507	6	31538302	31560299	111	40	453862	3.5533	0.00019	LTB	1	0.009387
ENSG00000149179	11	46948240	47195936	555	41	453862	3.5532	0.00019	C11orf49	1	0.009387
ENSG00000197381	21	46483768	46656478	774	45	453862	3.5513	0.000192	ADARB1	1	0.00942
ENSG00000169951	16	30555085	30579819	54	21	453862	3.5508	0.000192	ZNF764	1	0.00942
ENSG00000176658	17	30809540	31214195	1253	151	453862	3.5462	0.000195	MYO1D	1	0.009562
ENSG00000134533	12	15250717	15511609	832	71	453862	3.5367	0.000203	RERG	1	0.009867
ENSG00000183495	12	1.32E+08	1.33E+08	590	36	453862	3.5362	0.000203	EP400	1	0.009867
ENSG00000204764	5	1.7E+08	1.71E+08	1497	54	453862	3.5358	0.000203	RANBP17	1	0.009867
ENSG00000100889	14	24553262	24589807	106	42	453862	3.5348	0.000204	PCK2	1	0.009871
ENSG00000092978	1	2.18E+08	2.18E+08	819	101	453862	3.5335	0.000205	GPATCH2	1	0.009871
ENSG00000179979	4	1375340	1399780	79	27	453862	3.5332	0.000205	CRIPAK	1	0.009871
ENSG00000173276	21	43396940	43440496	203	45	453862	3.5326	0.000206	ZBTB21	1	0.009871
ENSG00000022567	8	1.42E+08	1.42E+08	625	89	453862	3.5322	0.000206	SLC45A4	1	0.009871
ENSG00000162869	2	48657737	48752525	470	49	453862	3.5312	0.000207	PPP1R21	1	0.009882
ENSG00000127054	1	1236965	1270071	134	29	453862	3.5267	0.00021	CPSF3L	1	0.010023
ENSG00000143952	2	64109280	64256206	676	58	453862	3.523	0.000213	VPS54	1	0.010137
ENSG00000105696	19	18708240	18741849	119	31	453862	3.5194	0.000216	TMEM59L	1	0.010251
ENSG00000196260	6	30889130	30909952	141	27	453862	3.517	0.000218	SFTA2	1	0.010316
ENSG00000088298	20	33693167	33875928	639	62	453862	3.5155	0.000219	EDEM2	1	0.010348
ENSG00000162222	11	62485541	62517765	92	21	453862	3.5117	0.000223	TTC9C	1	0.01047
ENSG00000187535	16	1550428	1672111	603	56	453862	3.51	0.000224	IFT140	1	0.010512
ENSG00000198756	1	1.84E+08	1.84E+08	544	87	453862	3.5078	0.000226	COLGALT2	1	0.010571
ENSG00000077254	1	78151672	78235537	224	57	453862	3.5059	0.000228	USP33	1	0.010621
ENSG00000183682	1	39947318	40001607	199	49	453862	3.5041	0.000229	BMP8A	1	0.010664
ENSG00000170390	4	1.51E+08	1.51E+08	826	70	453862	3.5005	0.000232	DCLK2	1	0.010757
ENSG00000116748	1	1.15E+08	1.15E+08	178	54	453862	3.5004	0.000232	AMPD1	1	0.010757
ENSG00000169957	16	30525325	30548142	37	25	453862	3.4993	0.000233	ZNF768	1	0.010774
ENSG00000173473	3	47616762	47833596	486	48	453862	3.4984	0.000234	SMARCC1	1	0.010779
ENSG00000157429	16	71488453	71608992	386	68	453862	3.4978	0.000235	ZNF19	1	0.010779
ENSG00000172568	5	1.57E+08	1.57E+08	113	13	453862	3.495	0.000237	FNDC9	1	0.010865
ENSG00000184486	6	99272580	99296660	92	24	453862	3.4938	0.000238	POU3F2	1	0.010888
ENSG00000077458	11	95492106	95533573	185	30	453862	3.4891	0.000242	FAM76B	1	0.011054
ENSG00000205758	21	34951647	35026232	180	69	453862	3.4839	0.000247	CRYZL1	1	0.011242
ENSG00000106018	7	1.59E+08	1.59E+08	720	61	453862	3.482	0.000249	VIPR2	1	0.011258
ENSG00000152592	4	88561459	88595513	140	28	453862	3.4817	0.000249	DMP1	1	0.011258
ENSG00000269490	6	33653196	33673474	119	19	453862	3.4815	0.000249	SBP1	1	0.011258
ENSG00000165323	11	92075262	92639618	2013	102	453862	3.4773	0.000253	FAT3	1	0.011409
ENSG00000140400	15	75638133	75670971	65	29	453862	3.4751	0.000255	MAN2C1	1	0.011474
ENSG00000197275	8	95374188	95497337	523	33	453862	3.474	0.000256	RAD54B	1	0.011493
ENSG00000147601	8	73911099	73970357	197	31	453862	3.4714	0.000259	TERF1	1	0.011579
ENSG00000095752	19	55865757	55891831	115	31	453862	3.4694	0.000261	IL11	1	0.011634
ENSG00000236980	3	49205065	49239291	75	17	453862	3.4681	0.000262	C3orf84	1	0.011661
ENSG00000130731	16	674429	696358	83	25	453862	3.4671	0.000263	C16orf13	1	0.011679
ENSG00000112333	6	1.08E+08	1.09E+08	112	52	453862	3.463	0.000267	NR2E1	1	0.01183
ENSG00000178222	4	1040038	1117350	432	26	453862	3.4611	0.000269	RNF212	1	0.011869
ENSG00000180720	11	46396640	46418107	42	23	453862	3.4605	0.00027	CHRM4	1	0.011869
ENSG00000182134	1	1.52E+08	1.52E+08	140	20	453862	3.4601	0.00027	TDRKH	1	0.011869
ENSG00000166407	11	8235851	8300263	310	72	453862	3.4579	0.000272	LMO1	1	0.01194
ENSG00000167107	17	48493519	48562206	233	52	453862	3.4545	0.000276	ACSF2	1	0.012041
ENSG00000141012	16	88870142	88933378	487	53	453862	3.4543	0.000276	GALNS	1	0.012041
ENSG00000105726	19	19746007	19784502	145	37	453862	3.4506	0.00028	ATP13A1	1	0.01218
ENSG00000120645	12	165931	297626	578	107	453862	3.4468	0.000284	IQSEC3	1	0.012305
ENSG00000139192	12	6550856	6585683	163	30	453862	3.4465	0.000284	TAPBPL	1	0.012305
ENSG00000142945	1	45195490	45243439	236	50	453862	3.4448	0.000286	KIF2C	1	0.012353
ENSG00000087206	5	1.76E+08	1.76E+08	585	31	453862	3.4412	0.00029	UIMC1	1	0.012491
ENSG00000132623	20	9956774	10047410	416	55	453862	3.4314	0.0003	ANKEF1	1	0.01289
ENSG00000124664	6	34495579	34534110	203	39	453862	3.4309	0.000301	SPDEF	1	0.01289
ENSG00000003756	3	50116341	50166454	104	22	453862	3.4306	0.000301	RBMS	1	0.01289
ENSG00000143951	2	63338518	64064977	2369	68	453862	3.4301	0.000302	WDPBP	1	0.01289
ENSG00000141551	17	80186899	80241607	189	48	453862	3.4294	0.000302	CSNK1D	1	0.012891
ENSG00000181896	19	19769605	19804318	127	37	453862	3.427	0.000305	ZNF101	1	0.012978
ENSG00000173391	12	10300902	10334737	160	19	453862	3.4255	0.000307	OLR1	1	0.013018
ENSG00000140598	15	82412571	82565104	657	57	453862	3.4245	0.000308	EFTUD1	1	0.013034
ENSG00000004766	7	92851653	92998338	367	69	453862	3.4226	0.00031	CCDC132	1	0.013094
ENSG00000189367	6	1.28E+08	1.28E+08	118	17	453862	3.4163	0.000317	KIAA0408	1	0.013375
ENSG00000103335	16	88771751	88861619	705	123	453862	3.4137	0.00032	PIEZ01	1	0.013469
ENSG00000165685	12	10313141	10354400	193	42	453862	3.411	0.000324	TMEM52B	1	0.013571
ENSG00000107404	1	1260656	1294730	142	25	453862	3.4081	0.000327	DVL1	1	0.013685

ENSG00000198520	1	45130364	45201263	298	92	453862	3.407	0.000328	C1orf228	1	0.013708
ENSG00000159409	1	1.52E+08	1.52E+08	93	24	453862	3.4024	0.000334	CELF3	1	0.013909
ENSG00000173421	3	49225861	49305537	172	37	453862	3.397	0.000341	CCDC36	1	0.014154
ENSG00000163590	3	1.6E+08	1.61E+08	1141	59	453862	3.394	0.000344	PPM1L	1	0.014279
ENSG00000185909	3	49199044	49223917	62	17	453862	3.3931	0.000346	KLHD8B	1	0.014294
ENSG00000184224	11	67360351	67384177	72	18	453862	3.3914	0.000348	C11orf72	1	0.014315
ENSG00000173227	11	66764249	66828334	200	28	453862	3.3912	0.000348	SYT12	1	0.014315
ENSG00000143319	1	1.57E+08	1.57E+08	73	29	453862	3.3903	0.000349	ISG20L2	1	0.014315
ENSG00000188659	15	82545151	82587271	144	39	453862	3.3902	0.000349	FAM154B	1	0.014315
ENSG00000162188	11	62465130	62486673	68	24	453862	3.3896	0.00035	GNG3	1	0.014315
ENSG00000251322	22	51102843	51181726	248	72	453862	3.3863	0.000354	SHANK3	1	0.014453
ENSG00000126778	14	61100133	61134977	92	29	453862	3.3839	0.000357	SIX1	1	0.014548
ENSG00000240857	2	18725989	18751946	77	34	453862	3.3782	0.000365	RDH14	1	0.01478
ENSG00000137288	6	33652070	33689504	223	31	453862	3.3778	0.000365	UQCQ2	1	0.01478
ENSG00000172489	11	56009676	56030698	75	11	453862	3.3777	0.000365	OR5T3	1	0.01478
ENSG00000175161	3	84998132	86133579	4590	115	453862	3.3762	0.000367	CADM2	1	0.01483
ENSG00000163710	3	1.43E+08	1.43E+08	329	69	453862	3.3746	0.00037	PCOLCE2	1	0.014852
ENSG00000153294	6	47643600	47699757	326	21	453862	3.3746	0.00037	GPR115	1	0.014852
ENSG00000129910	16	89228175	89271900	253	33	453862	3.3737	0.000371	CDH15	1	0.014864
ENSG00000131845	19	57852675	57881266	149	38	453862	3.373	0.000372	ZNF304	1	0.014872
ENSG00000135632	2	73431350	73464365	119	30	453862	3.3693	0.000377	SMYD5	1	0.015038
ENSG00000134851	4	56252124	56329564	330	40	453862	3.3687	0.000378	TMEM165	1	0.015038
ENSG00000169972	1	1233947	1257057	84	22	453862	3.3619	0.000387	PUSL1	1	0.01536
ENSG00000139190	12	6561403	6590153	145	21	453862	3.3616	0.000388	VAMP1	1	0.01536
ENSG00000174996	11	66014765	66045331	79	27	453862	3.3611	0.000388	KLC2	1	0.01536
ENSG00000144566	3	19978571	20036667	273	31	453862	3.3603	0.000389	RAB5A	1	0.015367
ENSG00000181693	11	56047529	56068566	82	15	453862	3.3581	0.000392	OR8H1	1	0.015459
ENSG00000188641	1	97533299	98396605	3159	200	453862	3.3556	0.000396	DPYD	1	0.015568
ENSG00000198837	1	1.54E+08	1.54E+08	82	17	453862	3.3488	0.000406	DENND4B	1	0.01592
ENSG00000145283	4	87734621	87780416	119	34	453862	3.3481	0.000407	SLC10A6	1	0.015926
ENSG00000237440	19	20708631	20758615	264	26	453862	3.3466	0.000409	ZNF737	1	0.015976
ENSG00000137338	6	28239314	28280326	166	35	453862	3.3454	0.000411	PGBD1	1	0.015983
ENSG00000135617	2	73445134	73470366	81	25	453862	3.345	0.000411	PRADC1	1	0.015983
ENSG00000169410	15	75749462	75881630	317	45	453862	3.3447	0.000412	PTPN9	1	0.015983
ENSG00000136942	9	1.28E+08	1.28E+08	78	17	453862	3.3439	0.000413	RPL35	1	0.015993
ENSG00000012504	12	1.01E+08	1.01E+08	381	54	453862	3.3391	0.00042	NR1H4	1	0.016207
ENSG00000148814	10	1.34E+08	1.34E+08	337	42	453862	3.3386	0.000421	LRRC27	1	0.016207
ENSG00000169981	3	44680219	44712283	57	26	453862	3.3385	0.000421	ZNF35	1	0.016207
ENSG00000183723	16	66638653	66740610	306	27	453862	3.3374	0.000423	CMTM4	1	0.016239
ENSG00000100325	22	30174597	30244271	266	36	453862	3.3365	0.000424	ASCC2	1	0.016257
ENSG00000183828	14	1.06E+08	1.06E+08	91	19	453862	3.333	0.00043	NUDT14	1	0.016394
ENSG00000116580	1	1.56E+08	1.56E+08	330	34	453862	3.333	0.00043	GON4L	1	0.016394
ENSG00000148655	10	77350998	78329925	3458	273	453862	3.3317	0.000432	C10orf11	1	0.016399
ENSG00000173611	9	1.28E+08	1.28E+08	692	55	453862	3.3309	0.000433	SCAI	1	0.016399
ENSG00000089094	12	1.22E+08	1.22E+08	441	60	453862	3.3301	0.000434	KDM2B	1	0.016399
ENSG00000100207	22	42546019	42749622	749	83	453862	3.3296	0.000435	TCF20	1	0.016399
ENSG00000197467	10	71551644	71734031	1040	176	453862	3.3289	0.000436	COL13A1	1	0.016399
ENSG00000163618	3	62374022	62871054	2342	173	453862	3.3289	0.000436	CADPS	1	0.016399
ENSG00000151067	12	2069952	2812108	3019	310	453862	3.3286	0.000436	CACNA1C	1	0.016399
ENSG00000196345	3	44586685	44634975	169	26	453862	3.3282	0.000437	ZKSCAN7	1	0.016399
ENSG00000127995	7	94128531	94196331	246	42	453862	3.3256	0.000441	CASD1	1	0.016518
ENSG00000152595	4	88732563	88777969	241	43	453862	3.3208	0.000449	MEPE	1	0.016773
ENSG00000169962	1	1256694	1280686	105	22	453862	3.3198	0.00045	TAS1R3	1	0.016797
ENSG00000127578	16	669239	694116	110	26	453862	3.3186	0.000452	WFIKKN1	1	0.016826
ENSG00000106868	9	1.15E+08	1.15E+08	561	87	453862	3.3182	0.000453	SUSD1	1	0.016826
ENSG00000138152	10	1.24E+08	1.24E+08	464	59	453862	3.3136	0.00046	BTBD16	1	0.017065
ENSG00000004534	3	49967440	50147478	459	37	453862	3.3131	0.000461	RBM6	1	0.017065
ENSG00000006128	7	97351220	97379784	144	23	453862	3.3083	0.000469	TAC1	1	0.017325
ENSG00000168615	8	38844388	38972663	413	44	453862	3.3069	0.000472	ADAM9	1	0.017367
ENSG00000089234	12	1.12E+08	1.12E+08	118	38	453862	3.3065	0.000472	BRAP	1	0.017367
ENSG00000224051	1	1250136	1274277	104	23	453862	3.3053	0.000474	GLTPD1	1	0.017405
ENSG00000165555	14	77850364	77899860	189	34	453862	3.3011	0.000482	NOXRED1	1	0.017635
ENSG00000111325	12	1.23E+08	1.23E+08	76	16	453862	3.3	0.000483	OGFOD2	1	0.01767
ENSG00000130779	12	1.23E+08	1.23E+08	581	50	453862	3.2981	0.000487	CLIP1	1	0.017755
ENSG00000005513	16	1021808	1046979	156	39	453862	3.2971	0.000488	SOX8	1	0.017778
ENSG00000157368	16	70603798	70704585	474	60	453862	3.2961	0.00049	IL34	1	0.017805
ENSG00000160741	1	1.54E+08	1.54E+08	78	29	453862	3.293	0.000496	CRTC2	1	0.017967
ENSG00000111275	12	1.12E+08	1.12E+08	140	33	453862	3.2923	0.000497	ALDH2	1	0.017979
ENSG00000100201	22	38869445	38913665	123	34	453862	3.2912	0.000499	DDX17	1	0.018014
ENSG00000100583	14	77833032	77867840	129	25	453862	3.2867	0.000507	SAMD15	1	0.018252
ENSG00000143570	1	1.54E+08	1.54E+08	68	24	453862	3.2857	0.000509	SLC39A1	1	0.018252
ENSG00000019995	10	1.27E+08	1.27E+08	194	31	453862	3.2855	0.000509	ZRANB1	1	0.018252
ENSG00000152430	2	1.99E+08	1.99E+08	168	33	453862	3.2849	0.00051	BOLL	1	0.018252

ENSG00000074695	18 56985055 57037194	230	30	453862	3.2847	0.00051 LMAN1	1	0.018252
ENSG00000169018	15 68560141 68598203	118	27	453862	3.2827	0.000514 FEM1B	1	0.01835
ENSG00000214415	7 80077987 80151336	242	47	453862	3.2813	0.000517 GNAT3	1	0.018405
ENSG00000141526	17 80176273 80229005	197	52	453862	3.2792	0.000521 SLC16A3	1	0.018505
ENSG00000118292	1 1.5E+08 1.5E+08	75	23	453862	3.2774	0.000524 C1orf54	1	0.018589
ENSG00000101544	18 77856915 77915406	240	30	453862	3.2763	0.000526 ADNP2	1	0.018613
ENSG00000114054	3 1.36E+08 1.36E+08	352	64	453862	3.2751	0.000528 PCCB	1	0.018613
ENSG00000136378	15 79041545 79113773	358	39	453862	3.2751	0.000528 ADAMTS7	1	0.018613
ENSG00000063978	4 2453947 2637047	816	71	453862	3.2748	0.000529 RNF4	1	0.018613
ENSG00000172482	2 2.42E+08 2.42E+08	216	28	453862	3.2738	0.000531 AGXT	1	0.018645
ENSG00000070669	7 97471430 97511854	209	32	453862	3.2637	0.00055 ASNS	1	0.019283
ENSG00000064225	3 98441080 98550045	431	48	453862	3.2603	0.000557 ST3GAL6	1	0.019479
ENSG00000117280	1 2.06E+08 2.06E+08	129	29	453862	3.2564	0.000564 RAB7L1	1	0.019653
ENSG00000156162	8 95721931 95816064	390	48	453862	3.2554	0.000566 DPY19L4	1	0.019653
ENSG00000145147	4 20244883 20632184	1557	177	453862	3.2553	0.000566 SLT2	1	0.019653
ENSG00000213996	19 19365173 19394200	118	23	453862	3.2552	0.000566 TM6SF2	1	0.019653
ENSG00000187456	17 34235070 34267777	143	17	453862	3.255	0.000567 RDM1	1	0.019653
ENSG00000205669	14 74067649 74096592	111	25	453862	3.253	0.000571 ACOT6	1	0.01976
ENSG00000166278	6 31855562 31923449	253	52	453862	3.2519	0.000573 C2	1	0.019798
ENSG00000157800	7 1.4E+08 1.4E+08	564	72	453862	3.25	0.000577 SLC37A3	1	0.019872
ENSG00000130703	20 60803580 60881268	333	39	453862	3.2497	0.000578 OSBP2	1	0.019872
ENSG00000232810	6 31533344 31556113	111	36	453862	3.2481	0.000581 TNF	1	0.019915
ENSG00000164393	6 47614172 47675533	377	18	453862	3.248	0.000581 GPR111	1	0.019915
ENSG00000178229	19 57821877 57852144	163	34	453862	3.2466	0.000584 ZNF543	1	0.01996
ENSG00000197713	2 2.11E+08 2.11E+08	88	40	453862	3.2461	0.000585 RPE	1	0.01996
ENSG00000044524	3 89146674 89541284	1359	71	453862	3.2458	0.000586 EPHA3	1	0.01996
ENSG00000116157	1 53058044 53084723	88	17	453862	3.2409	0.000596 GPX7	1	0.020246
ENSG00000089639	19 19730285 19764476	114	46	453862	3.2407	0.000596 GMIP	1	0.020246
ENSG00000136891	9 1.03E+08 1.03E+08	238	36	453862	3.2392	0.000599 TEX10	1	0.020314
ENSG00000103723	15 83318033 83388666	283	40	453862	3.2375	0.000603 AP3B2	1	0.020398
ENSG00000169499	8 38748753 38841428	313	86	453862	3.2344	0.00061 PLEKHA2	1	0.020582
ENSG00000184470	22 19853040 19939341	523	69	453862	3.2336	0.000611 TXNRD2	1	0.020604
ENSG00000132153	3 47834399 47901685	146	41	453862	3.2322	0.000614 DHX30	1	0.020667
ENSG00000036549	1 78018010 78159104	399	46	453862	3.2287	0.000622 ZZ3Z	1	0.02088
ENSG00000100319	22 30116945 30173000	248	38	453862	3.2248	0.00063 ZMAT5	1	0.02107
ENSG00000133275	19 1931188 1991337	290	34	453862	3.2247	0.000631 CSNK1G2	1	0.02107
ENSG00000136950	9 1.28E+08 1.28E+08	117	27	453862	3.2242	0.000632 ARPC5L	1	0.02107
ENSG00000138303	10 73846278 73986892	523	35	453862	3.224	0.000632 ASCC1	1	0.02107
ENSG00000146147	6 53784780 54141078	1207	94	453862	3.2216	0.000637 MLIP	1	0.021197
ENSG00000160883	5 1.76E+08 1.76E+08	141	51	453862	3.2212	0.000638 HK3	1	0.021197
ENSG00000147408	8 19251672 19625540	2108	146	453862	3.2184	0.000644 CSGALNACT1	1	0.021366
ENSG00000198752	14 1.03E+08 1.04E+08	518	62	453862	3.217	0.000648 CDC42BPB	1	0.021435
ENSG00000111249	12 1.11E+08 1.12E+08	873	95	453862	3.2113	0.000661 CUX2	1	0.021827
ENSG00000177051	19 46203887 46244162	95	42	453862	3.2098	0.000664 FBXO46	1	0.021895
ENSG00000163633	4 87787358 87867354	279	35	453862	3.2083	0.000668 C4orf36	1	0.021975
ENSG00000236287	11 10823621 10890343	265	30	453862	3.2054	0.000674 ZBED5	1	0.022153
ENSG00000198346	19 53960989 54016950	286	66	453862	3.2041	0.000678 ZNF813	1	0.022219
ENSG00000174957	11 55934094 55955032	69	12	453862	3.203	0.00068 OR5J2	1	0.022253
ENSG00000215545	20 29881015 29906388	109	27	453862	3.2026	0.000681 DEFB116	1	0.022253
ENSG00000214357	5 1.72E+08 1.72E+08	266	49	453862	3.2021	0.000682 NEURL1B	1	0.022253
ENSG00000254585	15 23878691 23901175	81	28	453862	3.2003	0.000686 MAGEL2	1	0.022348
ENSG00000128683	2 1.72E+08 1.72E+08	264	43	453862	3.1959	0.000697 GAD1	1	0.022653
ENSG00000060718	1 1.03E+08 1.04E+08	1330	54	453862	3.1924	0.000706 COL11A1	1	0.022869
ENSG00000185261	5 93478671 93964309	1189	159	453862	3.1921	0.000706 KIAA0825	1	0.022869
ENSG00000104442	8 66504694 66556442	250	28	453862	3.1902	0.000711 ARMC1	1	0.022977
ENSG00000033030	12 1.23E+08 1.23E+08	136	26	453862	3.1897	0.000712 ZCCHC8	1	0.022977
ENSG00000171680	1 6516152 6590121	295	55	453862	3.1829	0.000729 PLEKHG5	1	0.023485
ENSG00000136738	10 17676124 17767913	459	33	453862	3.182	0.000731 STAM	1	0.023519
ENSG00000130706	20 60867149 60893918	146	48	453862	3.1774	0.000743 ADRM1	1	0.023855
ENSG00000105968	7 44856390 44897682	158	31	453862	3.1754	0.000748 H2AFV	1	0.023891
ENSG00000144285	2 1.67E+08 1.67E+08	646	46	453862	3.1753	0.000748 SCN1A	1	0.023891
ENSG00000143376	1 1.52E+08 1.52E+08	259	39	453862	3.1752	0.000749 SNX27	1	0.023891
ENSG00000268156	14 77872741 77893115	79	25	453862	3.1749	0.00075 FKSG61	1	0.023891
ENSG00000157119	3 42717011 42744036	94	42	453862	3.1737	0.000753 KLHL40	1	0.02395
ENSG00000204482	6 31543901 31566686	126	45	453862	3.1728	0.000755 LST1	1	0.023981
ENSG00000265817	8 95380605 95459180	307	27	453862	3.1722	0.000756 FSBP	1	0.023987
ENSG00000163510	2 1.81E+08 1.81E+08	308	29	453862	3.1715	0.000758 CWC22	1	0.023999
ENSG00000187514	2 2.33E+08 2.33E+08	122	26	453862	3.1706	0.000761 PTMA	1	0.024035
ENSG00000047849	3 47882182 48140769	539	45	453862	3.17	0.000762 MAP4	1	0.024044
ENSG00000198961	5 1.09E+08 1.09E+08	464	32	453862	3.1685	0.000766 PJA2	1	0.024125
ENSG000000179603	7 1.26E+08 1.27E+08	3127	135	453862	3.167	0.00077 GRM8	1	0.024208
ENSG00000175206	1 11895766 11918402	117	25	453862	3.1642	0.000778 NPPA	1	0.0244
ENSG00000159131	21 34866238 34925797	172	46	453862	3.1621	0.000783 GART	1	0.024538

ENSG00000135736	16	57536090	57580511	219	48	453862	3.1556	0.000801	CCDC102A	1	0.025012
ENSG00000162961	2	32082878	32274881	677	53	453862	3.1549	0.000803	DPY30	1	0.025012
ENSG00000126524	7	66442664	66470588	85	34	453862	3.1548	0.000803	SBDS	1	0.025012
ENSG00000153885	19	34276838	34316668	155	50	453862	3.1542	0.000805	KCTD15	1	0.025012
ENSG00000118473	1	66989066	67223982	1055	43	453862	3.154	0.000805	SGIP1	1	0.025012
ENSG0000007545	16	1652326	1737909	299	43	453862	3.1517	0.000812	CRAMP1L	1	0.025165
ENSG00000164325	5	72459022	72480970	54	23	453862	3.1511	0.000813	TMEM174	1	0.025173
ENSG00000242485	1	1327288	1352693	99	21	453862	3.15	0.000816	MRPL20	1	0.025226
ENSG00000205726	21	35004706	35282165	880	88	453862	3.147	0.000825	ITSN1	1	0.02544
ENSG00000206052	18	67058291	67526323	2229	223	453862	3.1453	0.000829	DOK6	1	0.025482
ENSG00000169762	4	16152128	16239033	429	54	453862	3.1453	0.00083	TAPT1	1	0.025482
ENSG00000177034	5	79265584	79297082	106	22	453862	3.1448	0.000831	MTX3	1	0.025482
ENSG00000103227	16	893634	1041318	978	75	453862	3.1446	0.000832	LMF1	1	0.025482
ENSG00000140829	16	72117461	72156811	184	30	453862	3.1432	0.000836	DHX38	1	0.025507
ENSG00000136444	17	48546161	48573336	120	30	453862	3.143	0.000836	RSAD1	1	0.025507
ENSG00000132294	8	1.33E+08	1.33E+08	591	45	453862	3.1425	0.000838	EFR3A	1	0.025507
ENSG00000181718	11	55989490	56010737	70	11	453862	3.1419	0.000839	OR5T2	1	0.025507
ENSG0000043143	5	1.34E+08	1.34E+08	265	45	453862	3.1416	0.00084	JADE2	1	0.025507
ENSG00000205476	14	99967603	1E+08	536	65	453862	3.1414	0.000841	CCDC85C	1	0.025507
ENSG00000146441	2	63805743	63844331	112	27	453862	3.1408	0.000842	MDH1	1	0.025512
ENSG00000213654	6	32148543	32173300	94	32	453862	3.1396	0.000846	GPSM3	1	0.025575
ENSG00000221840	11	51401378	51422448	154	19	453862	3.1388	0.000848	OR4A5	1	0.025606
ENSG00000164941	8	95815539	95903974	382	38	453862	3.1359	0.000857	INTS8	1	0.025817
ENSG00000126214	14	1.04E+08	1.04E+08	606	51	453862	3.1348	0.00086	KLC1	1	0.025872
ENSG00000106609	7	66376212	66433538	228	36	453862	3.1323	0.000867	TMEM248	1	0.026014
ENSG00000109182	4	48978264	49074098	347	39	453862	3.1322	0.000868	CWH43	1	0.026014
ENSG00000174844	3	57317727	57540071	984	46	453862	3.1309	0.000871	DNAH12	1	0.026043
ENSG00000099385	16	30834947	30916281	130	25	453862	3.1309	0.000871	BCL7C	1	0.026043
ENSG00000083067	9	73133979	74071820	4191	190	453862	3.1291	0.000877	TRPM3	1	0.026155
ENSG00000184374	8	1.2E+08	1.2E+08	715	51	453862	3.1276	0.000881	COLEC10	1	0.026253
ENSG00000168209	10	74023678	74045794	83	22	453862	3.1269	0.000883	DDIT4	1	0.02627
ENSG00000118263	2	2.08E+08	2.08E+08	444	92	453862	3.1261	0.000886	KLF7	1	0.026301
ENSG00000133606	7	1.4E+08	1.4E+08	203	24	453862	3.1246	0.000889	MKRN1	1	0.026385
ENSG00000198373	16	69786209	69985644	812	48	453862	3.1226	0.000896	WWP2	1	0.026442
ENSG00000065371	3	1.24E+08	1.24E+08	162	46	453862	3.1226	0.000896	ROPN1	1	0.026442
ENSG00000099985	22	30648818	30672829	77	42	453862	3.1226	0.000896	OSM	1	0.026442
ENSG00000205581	21	40704241	40731573	116	21	453862	3.1205	0.000903	HMGN1	1	0.026584
ENSG00000080845	20	34884258	35167040	555	121	453862	3.1197	0.000905	DLGAP4	1	0.026613
ENSG00000178409	6	1.07E+08	1.07E+08	228	53	453862	3.1191	0.000907	BEND3	1	0.026627
ENSG00000139793	13	97863688	98056374	574	86	453862	3.1163	0.000916	MBNL2	1	0.02684
ENSG00000165714	12	1250013	12629840	540	68	453862	3.1154	0.000918	LOH12CR1	1	0.026875
ENSG00000100314	22	30106073	30137828	132	37	453862	3.1137	0.000924	CABP7	1	0.026951
ENSG00000247626	2	1.99E+08	1.99E+08	43	12	453862	3.1136	0.000924	MARS2	1	0.026951
ENSG00000184916	14	1.06E+08	1.06E+08	157	31	453862	3.1125	0.000927	JAG2	1	0.027008
ENSG00000185385	19	14981138	15002264	140	26	453862	3.1093	0.000938	OR7A17	1	0.027266
ENSG00000148604	10	85994809	86029716	153	47	453862	3.1071	0.000945	RGR	1	0.027394
ENSG00000185670	11	62505791	62531660	60	21	453862	3.1069	0.000945	ZBTB3	1	0.027394
ENSG00000145934	5	1.67E+08	1.68E+08	3454	362	453862	3.105	0.000951	TENM2	1	0.027528
ENSG00000143614	1	1.54E+08	1.54E+08	404	40	453862	3.1029	0.000958	GATAD2B	1	0.027654
ENSG00000185052	20	19183290	19713581	2330	178	453862	3.1027	0.000959	SLC24A3	1	0.027654
ENSG00000181785	11	55787895	55808869	175	9	453862	3.1014	0.000963	OR5AS1	1	0.027734
ENSG00000142959	1	45239257	45263377	78	24	453862	3.1001	0.000967	BEST4	1	0.027817
ENSG00000089022	12	1.12E+08	1.12E+08	235	20	453862	3.0993	0.00097	MAPKAPK5	1	0.027841
ENSG00000139220	12	81642045	82163332	1761	103	453862	3.0955	0.000982	PPFIA2	1	0.028154
ENSG00000165821	14	21979232	22015350	67	18	453862	3.0909	0.000998	SALL2	1	0.028554
ENSG00000148484	10	16622610	16869527	1089	122	453862	3.09	0.001001	RSU1	1	0.028596
ENSG00000116717	1	68140744	68164021	97	20	453862	3.0878	0.001008	GADD45A	1	0.028762
ENSG00000166037	11	95513129	95575857	307	28	453862	3.0873	0.00101	CEP57	1	0.028771
ENSG00000151445	14	77883018	77934295	248	43	453862	3.0863	0.001013	VIPAS39	1	0.028814
ENSG00000198270	12	1.12E+08	1.12E+08	266	19	453862	3.0848	0.001018	TMEM116	1	0.028914
ENSG00000075240	22	46961909	47085688	676	74	453862	3.0824	0.001027	GRAMD4	1	0.02911
ENSG00000185278	1	1.74E+08	1.74E+08	199	34	453862	3.0814	0.00103	ZBTB37	1	0.029156
ENSG00000115520	2	1.98E+08	1.98E+08	98	32	453862	3.0774	0.001044	COQ10B	1	0.029512
ENSG00000111640	12	6633093	6657537	99	24	453862	3.0765	0.001047	GAPDH	1	0.029556
ENSG00000100593	14	77930740	77975210	174	32	453862	3.0746	0.001054	ISM2	1	0.029691
ENSG00000198162	1	1.18E+08	1.18E+08	692	44	453862	3.0739	0.001057	MAN1A2	1	0.029724
ENSG00000183715	11	1.32E+08	1.33E+08	5392	436	453862	3.0725	0.001061	OPCML	1	0.029786
ENSG00000101489	18	34813010	35156000	1224	191	453862	3.0723	0.001062	CELF4	1	0.029786
ENSG00000243244	2	48746522	48836025	458	56	453862	3.0709	0.001067	STON1	1	0.029851
ENSG00000185420	1	2.46E+08	2.47E+08	4257	175	453862	3.0707	0.001068	SMYD3	1	0.029851
ENSG00000187486	11	17397406	17420878	126	26	453862	3.0693	0.001073	KCNJ11	1	0.029904
ENSG00000136918	9	1.28E+08	1.28E+08	96	17	453862	3.0692	0.001073	WDR38	1	0.029904
ENSG00000063438	5	294291	448406	767	73	453862	3.0688	0.001075	AHRR	1	0.029904

ENSG00000075711	3	1.97E+08	1.97E+08	1211	65	453862	3.0663	0.001084	DLG1	1	0.030111
ENSG000000183856	1	1.56E+08	1.57E+08	235	41	453862	3.0655	0.001087	IQGAP3	1	0.030151
ENSG000000132676	1	1.56E+08	1.56E+08	156	45	453862	3.0619	0.0011	DAP3	1	0.030471
ENSG000000156222	15	85417885	85528876	588	96	453862	3.0612	0.001102	SLC28A1	1	0.030486
ENSG000000123066	12	1.16E+08	1.17E+08	962	77	453862	3.0608	0.001104	MED13L	1	0.030486
ENSG000000127515	19	14941760	14962689	110	31	453862	3.0601	0.001106	OR7A10	1	0.030509
ENSG000000172154	11	55850753	55871762	151	9	453862	3.0579	0.001114	OR8I2	1	0.030642
ENSG000000158373	6	26148349	26181577	107	39	453862	3.0579	0.001115	HIST1H2BD	1	0.030642
ENSG000000144730	3	57114010	57214334	368	49	453862	3.054	0.001129	IL17RD	1	0.030999
ENSG000000181761	11	55879849	55900787	148	7	453862	3.0531	0.001132	OR8H3	1	0.031038
ENSG000000259511	15	84831242	84860986	18	9	453862	3.052	0.001137	UBE2Q2L	1	0.031109
ENSG00000064042	4	41351624	41712061	1483	143	453862	3.0505	0.001142	LIMCH1	1	0.031215
ENSG00000096433	6	33578142	33674351	594	74	453862	3.0494	0.001146	ITPR3	1	0.031283
ENSG000000143543	1	1.54E+08	1.54E+08	45	18	453862	3.0478	0.001153	JTB	1	0.031402
ENSG000000114646	3	47593729	47632282	98	32	453862	3.0467	0.001157	CSPG5	1	0.031478
ENSG000000171497	4	1.6E+08	1.6E+08	92	27	453862	3.0456	0.001161	PPID	1	0.031519
ENSG000000204334	2	1.72E+08	1.72E+08	142	19	453862	3.0454	0.001162	ERICH2	1	0.031519
ENSG000000100983	20	33506236	33553620	104	19	453862	3.0436	0.001169	GSS	1	0.031662
ENSG000000181273	11	56746347	56767342	85	27	453862	3.0395	0.001185	OR5AK2	1	0.032001
ENSG000000249915	5	261736	363971	483	40	453862	3.0394	0.001185	PDCD6	1	0.032001
ENSG000000167822	11	55894247	55915194	82	10	453862	3.039	0.001187	OR8J3	1	0.032001
ENSG000000181804	3	1.43E+08	1.44E+08	2437	252	453862	3.0359	0.001199	SLC9A9	1	0.032225
ENSG000000128342	22	30626436	30652840	62	29	453862	3.0358	0.0012	LIF	1	0.032225
ENSG000000161572	17	34251522	34280703	157	22	453862	3.0356	0.0012	LYZL6	1	0.032225
ENSG000000117713	1	27012524	27118595	256	29	453862	3.0329	0.001211	ARID1A	1	0.032425
ENSG000000139734	13	60229717	60748121	1870	59	453862	3.0324	0.001213	DIAPH3	1	0.032425
ENSG000000150261	11	56103421	56124507	83	12	453862	3.0324	0.001213	OR8K1	1	0.032425
ENSG000000105976	7	1.16E+08	1.16E+08	395	80	453862	3.0304	0.001221	MET	1	0.032591
ENSG000000157637	17	79208800	79279347	318	49	453862	3.0274	0.001233	SLC38A10	1	0.032866
ENSG000000111642	12	6669249	6726642	175	34	453862	3.0267	0.001236	CHD4	1	0.032892
ENSG000000187741	16	89793957	89893065	728	38	453862	3.026	0.001239	FANCA	1	0.032918
ENSG000000129292	8	1.34E+08	1.34E+08	289	30	453862	3.0256	0.001241	PHF20L1	1	0.032918
ENSG000000174903	11	66026004	66054963	74	23	453862	3.0215	0.001258	RAB1B	1	0.033323
ENSG000000143552	1	1.54E+08	1.54E+08	420	48	453862	3.0207	0.001261	NUP210L	1	0.033354
ENSG000000178773	16	89632176	89673654	196	52	453862	3.0195	0.001266	CPNE7	1	0.033443
ENSG000000172572	12	20512179	20847315	1326	139	453862	3.0175	0.001275	PDE3A	1	0.033619
ENSG000000243335	7	66083868	66286446	908	36	453862	3.0167	0.001278	KCTD7	1	0.033646
ENSG000000090061	14	99937506	1E+08	206	51	453862	3.0164	0.001279	CCNK	1	0.033646
ENSG000000057019	3	98504785	98630533	573	38	453862	3.0157	0.001282	DCBLD2	1	0.033671
ENSG000000164366	5	186986	228330	233	27	453862	3.0139	0.00129	CCDC127	1	0.033779
ENSG000000011105	12	3176521	3405730	1278	162	453862	3.0137	0.00129	TSPAN9	1	0.033779
ENSG000000197938	3	97991732	98012676	146	19	453862	3.0134	0.001292	OR5H2	1	0.033779
ENSG000000136935	9	1.28E+08	1.28E+08	282	41	453862	3.0115	0.0013	GOLGA1	1	0.03393
ENSG000000135414	12	56127064	56160911	67	32	453862	3.0112	0.001301	GDF11	1	0.03393
ENSG000000010310	19	46161502	46196982	153	37	453862	3.0096	0.001308	GIPR	1	0.034061
ENSG000000197329	2	64309786	64381588	237	42	453862	3.0084	0.001313	PELI1	1	0.034148
ENSG000000256771	19	19966695	20015483	216	37	453862	3.0061	0.001323	ZNF253	1	0.034351
ENSG000000163349	1	1.14E+08	1.15E+08	227	59	453862	3.0042	0.001331	HIPK1	1	0.034517
ENSG000000154710	7	66137151	66286451	668	33	453862	3.0037	0.001334	RABGEF1	1	0.03453
ENSG000000218819	2	21336789	21376144	153	35	453862	3.0007	0.001347	TDRD15	1	0.034815
ENSG000000186468	5	81559177	81584396	97	33	453862	2.9985	0.001356	RPS23	1	0.035018
ENSG000000196458	12	1.33E+08	1.34E+08	58	21	453862	2.9977	0.001365	ZNF605	1	0.035061
ENSG000000204291	9	1.02E+08	1.02E+08	641	93	453862	2.9945	0.001375	COL15A1	1	0.035385
ENSG000000204511	6	31486494	31508009	185	32	453862	2.9923	0.001385	MCCD1	1	0.035595
ENSG000000091490	4	25739055	25875382	528	104	453862	2.9889	0.0014	SEL1L3	1	0.035923
ENSG000000102886	16	30106131	30135177	69	33	453862	2.9886	0.001401	GDPD3	1	0.035923
ENSG000000118322	5	1.6E+08	1.6E+08	1286	120	453862	2.9874	0.001407	ATP10B	1	0.036008
ENSG000000173662	1	6605241	6649817	187	31	453862	2.9857	0.001415	TAS1R1	1	0.036066
ENSG000000143190	1	1.67E+08	1.67E+08	783	50	453862	2.9853	0.001416	POU2F1	1	0.036066
ENSG000000134490	18	20767108	21027925	661	88	453862	2.9853	0.001417	TMEM241	1	0.036066
ENSG000000140398	15	75629296	75657592	73	36	453862	2.9852	0.001417	NEIL1	1	0.036066
ENSG000000204351	6	31916857	31947532	128	45	453862	2.9848	0.001419	SKIV2L	1	0.036072
ENSG000000204475	6	31546672	31570762	140	50	453862	2.9829	0.001428	NCR3	1	0.036204
ENSG000000115641	2	1.06E+08	1.06E+08	414	81	453862	2.9828	0.001428	FHL2	1	0.036204
ENSG000000110700	11	17085936	17109334	87	26	453862	2.981	0.001437	RPS13	1	0.036367
ENSG000000169184	22	28134265	28207486	185	88	453862	2.9805	0.001439	MN1	1	0.036367
ENSG000000053438	20	36139617	36162092	70	26	453862	2.9801	0.001441	NNAT	1	0.036367
ENSG000000140931	16	66627777	66657795	96	26	453862	2.9787	0.001447	CMTM3	1	0.036442
ENSG000000149133	11	55751157	55772101	127	6	453862	2.9787	0.001448	OR5F1	1	0.036442
ENSG000000104081	15	40370091	40411093	91	42	453862	2.9736	0.001471	BMF	1	0.036957
ENSG000000131584	1	1217756	1254989	141	34	453862	2.9735	0.001472	ACAP3	1	0.036957
ENSG00000011405	11	17089277	17239530	457	54	453862	2.9726	0.001476	PIK3C2A	1	0.036988
ENSG000000185800	19	46276205	46306060	91	32	453862	2.9724	0.001477	DMWD	1	0.036988

ENSG00000254870	6 31487996 31524385	289	41	453862	2.9719	0.00148 ATP6V1G2-DDX39B	1	0.037002
ENSG00000162408	1 6571407 6624595	248	18	453862	2.9709	0.001485 NOL9	1	0.037057
ENSG00000226979	6 31529831 31552101	109	31	453862	2.9706	0.001486 LTA	1	0.037057
ENSG00000169946	8 1.06E+08 1.07E+08	1709	174	453862	2.9701	0.001488 ZFPM2	1	0.037057
ENSG00000204472	6 31572961 31594798	108	28	453862	2.9682	0.001498 AIF1	1	0.037191
ENSG00000105497	19 52064551 52102991	200	54	453862	2.9679	0.001499 ZNF175	1	0.037191
ENSG00000142937	1 45230923 45254451	84	29	453862	2.9678	0.0015 RPS8	1	0.037191
ENSG00000141655	18 59982520 60068516	439	87	453862	2.9658	0.00151 TNFRSF11A	1	0.03738
ENSG00000105339	8 1.42E+08 1.42E+08	338	76	453862	2.965	0.001513 DENND3	1	0.03739
ENSG00000198563	6 31487996 31520225	257	38	453862	2.9649	0.001514 DDX39B	1	0.03739
ENSG00000174579	3 1.36E+08 1.36E+08	174	71	453862	2.9624	0.001527 MSL2	1	0.037638
ENSG00000167792	11 67364323 67390006	91	17	453862	2.962	0.001528 NDUFV1	1	0.037638
ENSG00000242265	7 94275637 94309007	76	26	453862	2.9605	0.001536 PEG10	1	0.037755
ENSG0000011478	19 46185741 46217247	90	33	453862	2.9602	0.001537 QPCTL	1	0.037755
ENSG00000197312	1 15933995 16005539	225	21	453862	2.9578	0.001549 DD12	1	0.038006
ENSG00000181767	11 55862519 55883457	150	7	453862	2.9538	0.00157 OR8H2	1	0.03844
ENSG00000111011	12 1.23E+08 1.23E+08	116	25	453862	2.9534	0.001571 RSR2	1	0.03844
ENSG00000214513	2 73419386 73449641	112	24	453862	2.9527	0.001575 NOTO	1	0.038474
ENSG00000143578	1 1.54E+08 1.54E+08	62	23	453862	2.952	0.001578 CREB3L4	1	0.03851
ENSG00000175115	11 65827834 66022218	491	43	453862	2.9515	0.001581 PACS1	1	0.038527
ENSG00000124160	20 44679624 44728591	195	41	453862	2.9505	0.001586 NCOA5	1	0.038597
ENSG00000198087	6 47435525 47604999	624	34	453862	2.9466	0.001607 CD2AP	1	0.038991
ENSG00000167615	19 54950065 54983217	207	40	453862	2.9465	0.001607 LENG8	1	0.038991
ENSG00000147606	8 92211722 92420378	625	67	453862	2.9456	0.001612 SLC26A7	1	0.039033
ENSG00000111639	12 6591150 6613007	125	13	453862	2.9453	0.001613 MRPL51	1	0.039033
ENSG0000010295	12 6637541 6675239	140	37	453862	2.9447	0.001616 IFFO1	1	0.039033
ENSG00000134028	8 24231798 24273526	106	35	453862	2.9446	0.001617 ADAMDEC1	1	0.039033
ENSG00000163681	3 57731177 57924895	494	55	453862	2.9405	0.001639 SLMAP	1	0.039505
ENSG00000090372	19 47212764 47260251	173	46	453862	2.9389	0.001647 STRN4	1	0.039655
ENSG00000163075	2 1.2E+08 1.2E+08	386	46	453862	2.9362	0.001661 PCDP1	1	0.039941
ENSG00000099899	22 20089389 20114915	117	28	453862	2.935	0.001668 TRMT2A	1	0.040004
ENSG00000164828	7 845528 946072	748	77	453862	2.9349	0.001668 SUN1	1	0.040004
ENSG00000008869	2 37185526 37321485	541	57	453862	2.9341	0.001673 HEATR5B	1	0.040052
ENSG00000124900	11 55640773 55669286	117	9	453862	2.9336	0.001675 TRIM51	1	0.040052
ENSG00000187664	19 19356450 19383605	106	20	453862	2.9333	0.001677 HAPLN4	1	0.040052
ENSG00000168884	4 2733375 2768103	201	49	453862	2.9311	0.001689 TNIP2	1	0.040286
ENSG00000168916	5 1.24E+08 1.24E+08	548	74	453862	2.9299	0.001695 ZNF608	1	0.040383
ENSG00000198673	12 62092040 62682931	2558	164	453862	2.929	0.0017 FAM19A2	1	0.040447
ENSG00000147488	8 53013399 53383519	1361	133	453862	2.9266	0.001714 ST18	1	0.040688
ENSG00000174970	11 55724975 55745990	167	6	453862	2.9264	0.001715 OR10AG1	1	0.040688
ENSG00000181027	19 47239303 47290245	222	49	453862	2.9247	0.001724 FKRP	1	0.040857
ENSG00000163440	4 56412692 56468379	260	26	453862	2.9243	0.001726 PDCL2	1	0.040859
ENSG00000172487	11 56117691 56138764	98	14	453862	2.9237	0.001729 OR8J1	1	0.040877
ENSG0000006015	19 18689495 18713146	107	27	453862	2.9208	0.001746 C19orf60	1	0.041208
ENSG00000165325	11 93053137 93181653	513	38	453862	2.9175	0.001764 CCDC67	1	0.041596
ENSG00000079112	8 95129399 95239531	522	70	453862	2.9156	0.001775 CDH17	1	0.041796
ENSG00000145592	5 40815364 40845437	109	33	453862	2.9112	0.0018 RPL37	1	0.042309
ENSG00000185219	3 44471262 44529162	146	44	453862	2.911	0.001802 ZNF445	1	0.042309
ENSG00000158863	8 21936670 21972409	167	37	453862	2.9096	0.00181 FAM160B2	1	0.042446
ENSG00000156232	15 83468380 83513611	177	43	453862	2.9057	0.001832 WHAMM	1	0.042889
ENSG00000178381	7 1181707 1210395	264	28	453862	2.9055	0.001833 ZFAND2A	1	0.042889
ENSG00000132855	1 63053158 63081830	53	20	453862	2.9046	0.001838 ANGPTL3	1	0.042951
ENSG00000171495	5 40988119 41081444	488	56	453862	2.904	0.001842 MROH2B	1	0.042992
ENSG00000138821	4 1.03E+08 1.03E+08	888	75	453862	2.903	0.001848 SLC39A8	1	0.043024
ENSG00000175756	1 1299110 1320875	122	16	453862	2.9029	0.001849 AURKAIP1	1	0.043024
ENSG00000116138	1 15843308 15928874	378	27	453862	2.8992	0.00187 DNAJC16	1	0.043476
ENSG00000100897	14 24573404 24604451	82	21	453862	2.8958	0.001891 DCAF11	1	0.043898
ENSG00000137824	15 41018082 41058049	124	29	453862	2.894	0.001902 RMDN3	1	0.044102
ENSG00000100330	22 30269144 30436855	597	47	453862	2.8894	0.00193 MTMR3	1	0.044692
ENSG00000174851	11 66042051 66066641	47	20	453862	2.8888	0.001933 YIF1A	1	0.044714
ENSG00000138316	10 72422559 72532197	667	86	453862	2.8882	0.001937 ADAMTS14	1	0.044741
ENSG00000173566	8 21954383 21976932	105	22	453862	2.8878	0.00194 NUDT18	1	0.044741
ENSG00000143028	1 1.1E+08 1.1E+08	124	17	453862	2.8872	0.001944 SYPL2	1	0.044777
ENSG00000120253	6 1.5E+08 1.5E+08	139	18	453862	2.8855	0.001954 NUP43	1	0.044959
ENSG00000135392	12 56204744 56234608	76	36	453862	2.8846	0.00196 DNAJC14	1	0.045014
ENSG00000188266	15 78789906 78839714	196	27	453862	2.8843	0.001961 HYKK	1	0.045014
ENSG00000184076	22 30153358 30176402	91	20	453862	2.8837	0.001965 UQCRC10	1	0.045049
ENSG00000150625	4 1.77E+08 1.77E+08	1837	158	453862	2.8808	0.001983 GPM6A	1	0.045399
ENSG00000164949	8 95251481 95284578	164	32	453862	2.8799	0.001989 GEM	1	0.045436
ENSG00000132718	1 1.56E+08 1.56E+08	121	33	453862	2.8797	0.00199 SYT11	1	0.045436
ENSG00000101294	20 30092231 30167370	234	23	453862	2.8794	0.001992 HM13	1	0.045436
ENSG00000172464	11 56398942 56419947	70	18	453862	2.8766	0.00201 OR5AP2	1	0.045792
ENSG00000109180	4 48797229 48873834	158	41	453862	2.8751	0.00202 OCIAD1	1	0.045927

ENSG00000128573	7	1.14E+08	1.14E+08	1890	134	453862	2.8748	0.002021	FOXP2	1	0.045927
ENSG00000162959	2	32080129	32246299	557	45	453862	2.8738	0.002028	MEMO1	1	0.046024
ENSG00000106346	7	6134515	6211195	354	44	453862	2.8712	0.002044	USP42	1	0.046337
ENSG00000215695	1	15976364	15998217	62	11	453862	2.8707	0.002048	RSC1A1	1	0.046358
ENSG00000165983	10	16468942	16565736	427	40	453862	2.8691	0.002058	PTER	1	0.04654
ENSG00000196098	3	98062698	98083663	78	26	453862	2.8661	0.002078	OR5K4	1	0.046921
ENSG00000188315	3	49296035	49325342	61	23	453862	2.865	0.002085	C3orf62	1	0.047018
ENSG0000068781	2	48747064	49013654	1287	119	453862	2.8639	0.002092	STON1-GTF2A1L	1	0.047127
ENSG00000187612	11	55671126	55692058	176	8	453862	2.8627	0.0021	OR5W2	1	0.047253
ENSG00000111641	12	6656029	6687857	90	30	453862	2.8622	0.002104	NOP2	1	0.047273
ENSG00000115504	2	62890986	63283622	905	94	453862	2.8609	0.002112	EHBP1	1	0.047406
ENSG00000084674	2	21214301	21276945	210	78	453862	2.8604	0.002116	APOB	1	0.047423
ENSG00000249860	10	57348750	57370488	74	16	453862	2.859	0.002125	MTRNR2L5	1	0.047548
ENSG00000106415	7	7998425	8143902	736	56	453862	2.8588	0.002127	GLCC1	1	0.047548
ENSG00000114279	3	1.92E+08	1.92E+08	2672	224	453862	2.8561	0.002144	FGF12	1	0.047882
ENSG00000116771	1	15888848	15921605	179	23	453862	2.8557	0.002147	AGMAT	1	0.047882
ENSG00000189298	6	28307691	28346947	201	33	453862	2.8554	0.002149	ZKSCAN3	1	0.047882
ENSG00000250741	2	18726811	18780830	165	41	453862	2.85	0.002186	NT5C1B-RDH14	1	0.048583
ENSG00000185013	2	18727050	18780838	165	41	453862	2.85	0.002186	NT5C1B	1	0.048583
ENSG00000163629	4	87505468	87746324	865	24	453862	2.8485	0.002197	PTPN13	1	0.048693
ENSG00000100644	14	62152231	62224976	235	47	453862	2.8484	0.002197	HIF1A	1	0.048693
ENSG00000181698	11	56033029	56054146	73	14	453862	2.8481	0.002199	OR5T1	1	0.048693
ENSG00000127990	7	94204542	94295521	228	42	453862	2.8473	0.002205	SGCE	1	0.048762
ENSG00000203760	6	1.27E+08	1.27E+08	57	30	453862	2.8465	0.00221	CENPW	1	0.048779
ENSG00000176293	19	58560607	58607677	152	37	453862	2.8461	0.002213	ZNF135	1	0.048779
ENSG00000117425	1	45275516	45318735	186	36	453862	2.846	0.002214	PTCH2	1	0.048779
ENSG00000165443	10	60926350	61017534	341	31	453862	2.8455	0.002217	PHYHPL	1	0.048793
ENSG00000105519	19	5901718	5925888	109	35	453862	2.8446	0.002223	CAPS	1	0.048868
ENSG00000198646	20	33274722	33423452	373	39	453862	2.8437	0.002229	NCOA6	1	0.048893
ENSG00000110921	12	1.1E+08	1.1E+08	206	36	453862	2.8435	0.002231	MVK	1	0.048893
ENSG00000078114	10	21058902	21473116	1732	143	453862	2.8433	0.002232	NEBL	1	0.048893
ENSG00000150991	12	1.25E+08	1.25E+08	94	28	453862	2.8421	0.002241	UBC	1	0.049025

Supplementary Table 8C. Gene sets defined by MAGMA

SET	NGENES	BETA	BETA_STD_SE	P	FULL_NAME	Bonferroni FDR
Curated_g	53	1.14	0.0614	0.253	3.44E-06 Curated_gene_sets:nikolsky_breast_cancer_16q24_amplicon	0.037465 0.019822
GO_bp:go	16	0.994	0.0295	0.225	4.92E-06 GO_bp:go_positive_regulation_of_neurotransmitter_transport	0.053584 0.019822
GO_bp:go	21	0.97	0.0329	0.22	5.46E-06 GO_bp:go_central_nervous_system_projection_neuron_axono	0.059465 0.019822
GO_bp:go	1355	0.11	0.0289	0.0272	2.67E-05 GO_bp:go_neurogenesis	0.29079 0.065999
GO_bp:go	26	0.786	0.0297	0.196	3.03E-05 GO_bp:go_central_nervous_system_neuron_axonogenesis	0.329997 0.065999
GO_bp:go	22	0.772	0.0268	0.198	4.87E-05 GO_bp:go_ncrna_catabolic_process	0.530392 0.078601
Curated_g	39	0.58	0.0268	0.152	6.98E-05 Curated_gene_sets:jaeger_metastasis_up	0.760192 0.078601
GO_mf:go	782	0.137	0.0278	0.0362	7.60E-05 GO_mf:go_Regulatory_region_nucleic_acid_binding	0.827716 0.078601
GO_bp:go	926	0.123	0.027	0.0326	8.16E-05 GO_bp:go_chromosome_organization	0.888706 0.078601
GO_bp:go	13	1.01	0.027	0.268	8.16E-05 GO_bp:go_pre_mirna_processing	0.888706 0.078601
GO_bp:go	722	0.139	0.0271	0.0369	8.71E-05 GO_bp:go_Regulation_of_nervous_system_development	0.948606 0.078601
Curated_g	190	0.257	0.0261	0.0685	8.89E-05 Curated_gene_sets:pal_prmt5_targets_up	0.96821 0.078601
GO_bp:go	23	0.755	0.0268	0.202	9.60E-05 GO_bp:go_neurotrophin_signaling_pathway	1 0.078601
GO_bp:go	1413	0.1	0.0268	0.027	0.000102 GO_bp:go_negative_regulation_of_gene_expression	1 0.078601
GO_bp:go	99	0.354	0.0261	0.0959	0.000112 GO_bp:go_camera_type_eye_morphogenesis	1 0.078601
GO_bp:go	336	0.192	0.0258	0.0522	0.000118 GO_bp:go_Regulation_of_membrane_potential	1 0.078601
GO_bp:go	1420	0.0982	0.0264	0.0268	0.000123 GO_bp:go_negative_regulation_of_nitrogen_compound_metab	1 0.078601
GO_bp:go	290	0.204	0.0256	0.056	0.000134 GO_bp:go_modulation_of_synaptic_transmission	1 0.080841
Curated_g	55	0.491	0.0269	0.136	0.000155 Curated_gene_sets:delaserna_myod_targets_dn	1 0.088962

Supplementary Table 9A. Correlated DHS sites for SPOCK2 gene according to <http://dnase.genome.duke.edu/> database.

<http://dnase.genome.duke.edu/geneDetail.php?ensemblID=ENSG00000107742>

Positive Correlation

Location	Connect	Cluster	Pvalue
chr10: 73844040-ENSG00000107742		2072	0
chr10: 73843605-ENSG00000107742		2072	0.001
chr10: 73855065-ENSG00000107742		2072	0.001
chr10: 73844245-ENSG00000107742		2072	0.001
chr10: 73843885-ENSG00000107742		2072	0.001
chr10: 73842945-ENSG00000107742		1755	0.002
chr10: 73848225-ENSG00000107742		1258	0.005
chr10: 73868305-ENSG00000107742		1754	0.005
chr10: 73840025-ENSG00000107742		1054	0.008
chr10: 73846885-ENSG00000107742		1306	0.009
chr10: 73847385-ENSG00000107742		1259	0.009
chr10: 73812385-ENSG00000107742		1755	0.011
chr10: 73799445-ENSG00000107742		1970	0.011
chr10: 73848000-ENSG00000107742		2122	0.011
chr10: 73729085-ENSG00000107742		860	0.012
chr10: 73915325-ENSG00000107742		2001	0.012
chr10: 73794085-ENSG00000107742		1355	0.014
chr10: 73867640-ENSG00000107742		2017	0.014
chr10: 73811685-ENSG00000107742		1755	0.015
chr10: 73848925-ENSG00000107742		582	0.019
chr10: 73869385-ENSG00000107742		1777	0.019
chr10: 73784920-ENSG00000107742		1079	0.019
chr10: 73760225-ENSG00000107742		1079	0.021
chr10: 73821125-ENSG00000107742		1079	0.021
chr10: 73847825-ENSG00000107742		1157	0.022
chr10: 73848540-ENSG00000107742		2122	0.022
chr10: 73894700-ENSG00000107742		2020	0.024

Negative Correlation

Location	Connect	Cluster	Pvalue
chr10: 73769180-ENSG00000107742		1150	0.001
chr10: 73935060-ENSG00000107742		2220	0.003
chr10: 73893400-ENSG00000107742		272	0.004
chr10: 73857465-ENSG00000107742		1439	0.004
chr10: 73769705-ENSG00000107742		1395	0.004
chr10: 73745620-ENSG00000107742		1443	0.004
chr10: 73769340-ENSG00000107742		546	0.005
chr10: 73758700-ENSG00000107742		749	0.007
chr10: 73735700-ENSG00000107742		186	0.007
chr10: 73723120-ENSG00000107742		1375	0.011
chr10: 73786620-ENSG00000107742		1547	0.014
chr10: 73740160-ENSG00000107742		713	0.023
chr10: 73734300-ENSG00000107742		898	0.023

Supplementary Table 9B. Correalated DHS sites for CHST3 gene according to <http://dnase.genome.duke.edu/> database.

<http://dnase.genome.duke.edu/geneDetail.php?ensemblID=ENSG00000122863>

Positive Correlation

Location	Connect	Cluster	Pvalue
chr10: 73769340-73769490	ENSG00001	546	0.003
chr10: 73735700-73735850	ENSG00001	186	0.003
chr10: 73728540-73728690	ENSG00001	1809	0.004
chr10: 73726160-73726310	ENSG00001	1145	0.004
chr10: 73735900-73736050	ENSG00001	1145	0.004
chr10: 73769180-73769330	ENSG00001	1150	0.004
chr10: 73724980-73725130	ENSG00001	944	0.004
chr10: 73857620-73857770	ENSG00001	545	0.004
chr10: 73768900-73769050	ENSG00001	2294	0.004
chr10: 73631180-73631330	ENSG00001	250	0.004
chr10: 73628140-73628290	ENSG00001	748	0.004
chr10: 73769520-73769670	ENSG00001	1249	0.004
chr10: 73769705-73769855	ENSG00001	1395	0.007
chr10: 73786620-73786770	ENSG00001	1547	0.007
chr10: 73728300-73728450	ENSG00001	1651	0.007
chr10: 73798600-73798750	ENSG00001	1523	0.007
chr10: 73857465-73857615	ENSG00001	1439	0.007
chr10: 73734300-73734450	ENSG00001	898	0.011
chr10: 73687880-73688030	ENSG00001	2356	0.011
chr10: 73857885-73858035	ENSG00001	1189	0.011
chr10: 73759065-73759215	ENSG00001	1517	0.013
chr10: 73735185-73735335	ENSG00001	1520	0.013
chr10: 73723120-73723270	ENSG00001	1375	0.013
chr10: 73726005-73726155	ENSG00001	1520	0.013
chr10: 73741285-73741435	ENSG00001	1715	0.013
chr10: 73758905-73759055	ENSG00001	2104	0.014
chr10: 73734660-73734810	ENSG00001	1415	0.016
chr10: 73730700-73730850	ENSG00001	1702	0.018
chr10: 73746680-73746830	ENSG00001	1592	0.018
chr10: 73624960-73625110	ENSG00001	560	0.018
chr10: 73735400-73735550	ENSG00001	1472	0.019
chr10: 73768580-73768730	ENSG00001	1777	0.019
chr10: 73745620-73745770	ENSG00001	1443	0.022
chr10: 73759240-73759390	ENSG00001	2333	0.022
chr10: 73725545-73725695	ENSG00001	1758	0.022

Negative Correlation

Location	Connect	Cluster	Pvalue
chr10: 73638400-73638550	ENSG00001	870	0.004
chr10: 73633480-73633630	ENSG00001	72	0.01
chr10: 73847385-73847535	ENSG00001	1259	0.01
chr10: 73669260-73669410	ENSG00001	2168	0.01
chr10: 73693500-73693650	ENSG00001	2170	0.01
chr10: 73848225-73848375	ENSG00001	1258	0.012
chr10: 73819640-73819790	ENSG00001	217	0.012
chr10: 73744620-73744770	ENSG00001	218	0.013
chr10: 73835345-73835495	ENSG00001	265	0.013
chr10: 73633765-73633915	ENSG00001	217	0.017
chr10: 73634620-73634770	ENSG00001	514	0.019
chr10: 73848000-73848150	ENSG00001	2122	0.021

chr10: 73848380-73848530	ENSG00001	1558	0.021
chr10: 73638560-73638710	ENSG00001	2113	0.021
chr10: 73833665-73833815	ENSG00001	1208	0.022
chr10: 73634460-73634610	ENSG00001	367	0.022
chr10: 73814800-73814950	ENSG00001	320	0.022
chr10: 73839240-73839390	ENSG00001	2165	0.022
chr10: 73819805-73819955	ENSG00001	511	0.023

Supplementary Table 9C. Joint table of correlated DHS sites for SPOCK2 and CHST3 genes ordered by the starting position.

Legend

Gene: 1 - corresponds to SPOCK2, 2 - corresponds to CHST3.

Correalation: p -positive, n - negative.

The overlaped regons are marked by yellow and green.

Green color highlights the DHS site with close SNP from credible set. It corresponds to SOM #1443 (<http://dnase.genome.duke.edu/clusterDetail.php?clusterID=1443>).

Other SNPs from credible set are highlighted by blue.

Locus	Gene	Correalation	Start	End	Length	Diff to Clos	Diff to Clos	Position	rsID
chr10: 73624960-73625110	2	p	73624960	73625110	150				
chr10: 73628140-73628290	2	p	73628140	73628290	150				
chr10: 73631180-73631330	2	p	73631180	73631330	150				
chr10: 73633480-73633630	2	n	73633480	73633630	150				
chr10: 73633765-73633915	2	n	73633765	73633915	150				
chr10: 73634460-73634610	2	n	73634460	73634610	150				
chr10: 73634620-73634770	2	n	73634620	73634770	150				
chr10: 73638400-73638550	2	n	73638400	73638550	150				
chr10: 73638560-73638710	2	n	73638560	73638710	150				
chr10: 73669260-73669410	2	n	73669260	73669410	150				
chr10: 73687880-73688030	2	p	73687880	73688030	150				
chr10: 73693500-73693650	2	n	73693500	73693650	150				
chr10: 73723120-73723270	1	n	73723120	73723270	150				
chr10: 73723120-73723270	2	p	73723120	73723270	150				
chr10: 73724980-73725130	2	p	73724980	73725130	150				
chr10: 73725545-73725695	2	p	73725545	73725695	150				
chr10: 73726005-73726155	2	p	73726005	73726155	150				
chr10: 73726160-73726310	2	p	73726160	73726310	150				
chr10: 73728300-73728450	2	p	73728300	73728450	150				
chr10: 73728540-73728690	2	p	73728540	73728690	150				
chr10: 73729085-73729235	1	p	73729085	73729235	150				
chr10: 73730700-73730850	2	p	73730700	73730850	150				
chr10: 73734300-73734450	1	n	73734300	73734450	150				
chr10: 73734300-73734450	2	p	73734300	73734450	150				
chr10: 73734660-73734810	2	p	73734660	73734810	150				
chr10: 73735185-73735335	2	p	73735185	73735335	150				
chr10: 73735400-73735550	2	p	73735400	73735550	150				
chr10: 73735700-73735850	1	n	73735700	73735850	150				
chr10: 73735700-73735850	2	p	73735700	73735850	150				
chr10: 73735900-73736050	2	p	73735900	73736050	150				
chr10: 73740160-73740310	1	n	73740160	73740310	150				
chr10: 73741285-73741435	2	p	73741285	73741435	150	-421	-271	73741706	rs2091331
chr10: 73744620-73744770	2	n	73744620	73744770	150				
chr10: 73745620-73745770	1	n	73745620	73745770	150	144	294	73745476	rs1006974
chr10: 73745620-73745770	2	p	73745620	73745770	150				
chr10: 73746680-73746830	2	p	73746680	73746830	150				
chr10: 73758700-73758850	1	n	73758700	73758850	150				
chr10: 73758905-73759055	2	p	73758905	73759055	150				
chr10: 73759065-73759215	2	p	73759065	73759215	150				
chr10: 73759240-73759390	2	p	73759240	73759390	150	-5269	-5119		
chr10: 73760225-73760375	1	p	73760225	73760375	150	-4284	-4134	73764509	rs6480592
chr10: 73768580-73768730	2	p	73768580	73768730	150	4071	4221		
chr10: 73768900-73769050	2	p	73768900	73769050	150	4391	4541		
chr10: 73769180-73769330	1	n	73769180	73769330	150	4671	4821		
chr10: 73769180-73769330	2	n	73769180	73769330	150				
chr10: 73769340-73769490	1	n	73769340	73769490	150				
chr10: 73769340-73769490	2	n	73769340	73769490	150				
chr10: 73769520-73769670	2	n	73769520	73769670	150				
chr10: 73769705-73769855	1	n	73769705	73769855	150				
chr10: 73769705-73769855	2	n	73769705	73769855	150				
chr10: 73784920-73785070	1	n	73784920	73785070	150				
chr10: 73786620-73786770	1	n	73786620	73786770	150				
chr10: 73786620-73786770	2	n	73786620	73786770	150				
chr10: 73794085-73794235	1	n	73794085	73794235	150				
chr10: 73798600-73798750	2	n	73798600	73798750	150	-4275	-4125		
chr10: 73799445-73799595	1	n	73799445	73799595	150	-3430	-3280	73802875	rs1269600
chr10: 73811685-73811835	1	n	73811685	73811835	150	5873	6023	73805812	rs1668159
chr10: 73812385-73812535	1	n	73812385	73812535	150	6573	6723		
chr10: 73814800-73814950	2	n	73814800	73814950	150				
chr10: 73819640-73819790	2	n	73819640	73819790	150				
chr10: 73819805-73819955	2	n	73819805	73819955	150				
chr10: 73821125-73821275	1	n	73821125	73821275	150	-4527	-4377	73825652	rs1668169
chr10: 73833665-73833815	2	n	73833665	73833815	150	806	956	73832859	rs896074
chr10: 73835345-73835495	2	n	73835345	73835495	150	2486	2636		
chr10: 73839240-73839390	2	n	73839240	73839390	150				
chr10: 73840025-73840295	1	n	73840025	73840295	270				
chr10: 73842945-73843095	1	n	73842945	73843095	150				
chr10: 73843605-73843755	1	n	73843605	73843755	150				
chr10: 73843885-73844035	1	n	73843885	73844035	150				

chr10: 73844040-73844190
chr10: 73844245-73844395
chr10: 73846885-73847035
chr10: 73847385-73847535
chr10: 73847385-73847535
chr10: 73847825-73847975
chr10: 73848000-73848150
chr10: 73848000-73848150
chr10: 73848225-73848375
chr10: 73848225-73848375
chr10: 73848380-73848530
chr10: 73848540-73848690
chr10: 73848925-73849075
chr10: 73855065-73855215
chr10: 73857465-73857615
chr10: 73857465-73857615
chr10: 73857620-73857770
chr10: 73857885-73858035
chr10: 73867640-73867790
chr10: 73868305-73868455
chr10: 73869385-73869535
chr10: 73893400-73893550
chr10: 73894700-73894850
chr10: 73915325-73915475
chr10: 73935060-73935210

1	n	73844040	73844190	150				
1	n	73844245	73844395	150				
1	n	73846885	73847035	150				
1	n	73847385	73847535	150				
2	n	73847385	73847535	150				
1	n	73847825	73847975	150				
1	n	73848000	73848150	150				
2	n	73848000	73848150	150				
1	n	73848225	73848375	150				
2	n	73848225	73848375	150				
2	n	73848380	73848530	150				
1	n	73848540	73848690	150				
1	n	73848925	73849075	150				
1	n	73855065	73855215	150				
1	n	73857465	73857615	150				
2	n	73857465	73857615	150				
2	n	73857620	73857770	150				
2	n	73857885	73858035	150				
1	n	73867640	73867790	150				
1	n	73868305	73868455	150				
1	n	73869385	73869535	150				
1	n	73893400	73893550	150				
1	n	73894700	73894850	150				
1	n	73915325	73915475	150				
1	n	73935060	73935210	150				